

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 11, 2005, 09:35:34 ; Search time 39 Seconds
(without alignments)
61.677 Million cell updates/sec

Title: SEQ1
Perfect score: 105
Sequence: 1 axaaaeakkaakyaeeakkaakaxa 25

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	67.6	924	2	T06636
2	65	61.9	168	2	T34804
3	63	60.0	179	2	F97683
4	63	60.0	179	2	AF2908
5	63	60.0	421	2	JV0057
6	60	57.1	177	2	B87294
7	58	55.2	354	1	GNVSR
8	58	55.2	375	2	A71625
9	57	54.3	394	2	G85576
10	57	54.3	394	2	G85576
11	57	54.3	909	2	T06635
12	56	53.3	101	2	H5099
13	56	53.3	228	2	B87612
14	56	53.3	347	2	B83525
15	56	53.3	356	2	A82152
16	56	53.3	564	2	AH2328
17	56	53.3	592	1	IKERCA
18	55	52.4	97	2	S02376
19	55	52.4	110	2	T37490
20	55	52.4	555	2	S04909
21	55	52.4	1110	2	IS1116
22	55	52.4	1147	2	T35781
23	55	51.9	1203	2	C95229
24	54.5	51.9	1216	2	G98093
25	54	51.4	217	2	A26721
26	54	51.4	310	2	T34809
27	54	51.4	643	1	T07064
28	54	51.4	1156	2	T34852
29	54	51.4	1687	1	A39638

30	53.5	51.0	45	2	A05163	antifreeze protein
31	53.5	51.0	846	2	S52418	GTP-binding regula
32	53	50.5	40	1	FDPI8G	antifreeze protein
33	53	50.5	205	2	S19114	cgr-1 protein - C
34	53	50.5	376	2	AG0592	toia protein (impo
35	53	50.5	388	2	AC0138	toia colicin impor
36	53	50.5	893	2	T38147	dolichyl-phosphate
37	52.5	50.0	1175	2	H83437	hypothetical prote
38	52	49.5	97	2	G60110	repetitive protein
39	52	49.5	147	2	D86189	hypothetical prote
40	52	49.5	192	2	T26386	hypothetical prote
41	52	49.5	210	2	A25350	histone H1 - sea u
42	52	49.5	248	1	HSUR1P	histone H1, gonada
43	52	49.5	288	2	S58219	ABA-inducible prot
44	52	49.5	294	2	S32234	transcription anti
45	52	49.5	294	2	S41061	probable transcrip

ALIGNMENTS

RESULT 1
T06636
hypothetical protein T20K18.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06636
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dikse, W.; Stiekema, W.; Bancroft, I.; Mew,
submitted to the Protein Sequence Database, April 1999
A:Reference number: 215790
A:Accession: T06636
A:Molecule type: DNA
A:Residues: 1-924 <BEV>
A:Cross-references: UNIPROT:Q9SU08; EMBL:AL049640; GSPDB:GN00062; ATSP:T20K18.130
C:Genetics:
A:Gene: T20K18.130
A:Map position: 4
A:Introns: 209/2; 699/3; 753/3; 785/2; 807/2; 853/3; 912/3

Query Match 67.6%; Score 71; DB 2; Length 924;
Best Local Similarity 68.0%; Pred. No. 0.7;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 1 AXAAAEAKKAYAAAEAKKAKAXA 25
Db 603 AAAGARDKAAKAAAEAREKAKKAA 627

RESULT 2
T34804
hypothetical protein SC2E1.36 SC2E1.36 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34804
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A:Reference number: 221557
A:Accession: T34804
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-168 <MUR>
A:Cross-references: UNIPROT:O69907; EMBL:AL023797; PIDN:CAA19411.1; GSPDB:GN00070; SCOEID:
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEID:SC2E1.36

Query Match 61.9%; Score 65; DB 2; Length 168;
Best Local Similarity 62.5%; Pred. No. 0.8;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Cy 1 AXAAAEAKKAYAAAEAKKAKAX 24
Db 15:||||| : |||:|

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C/Accession: A40787
R/Rolt, M.B.; Tremaine, J.H.; Rochon, D.M.
Virology 185, 468-472, 1991
A>Title: Comparison of the 5' and 3' termini of tomato ringspot virus RNA1 and RNA2: evi
F/270/Binding site: carbohydrate (Asn) (covalent) #status predicted
A/Reference number: A40787; MUID:92024112; PMID:1926788
A/Accession: A40787
A/Molecule type: genomic RNA
A/Residues: 1-354 <ROT>
A/Cross-references: UNIPROT:P29150; GB:M73822; NID:G335267; PIDN:AAA47941.1; PID:G555406
C/Genetics:
A/Map position: segment 1
C/Superfamily: tomato ringspot virus genome polyprotein
C/Keywords: glycoprotein; polyprotein
F/270/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.2%; Score 58; DB 1; Length 354;
Best Local Similarity 70.0%; Pred. No. 9.7;
Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 6 AEAARAAEAARAAEAARAAEA 25
DB 180 ARKAAKAAARAAARAAARAA 199

RESULT 8
A71625
rifin PRB0035C - malaria parasite (Plasmodium falciparum)
C/Species: Plasmodium falciparum
C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C/Accession: A71625
R/Gardner, M.J.; Tetteilin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Science 282, 1126-1132, 1998
A>Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A/Reference number: A71600; MUID:99021743; PMID:9804551
A/Accession: A71625
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-375 <GAR>
A/Cross-references: UNIPROT:O96113; GB:AE001367; GB:AE001362; NID:G3845074; PIDN:AAC7179
A/Experimental source: clone 3D7
C/Genetics:
A/Gene: PFB0035C
C/Superfamily: Plasmodium falciparum rifin PRB1005W

Query Match 55.2%; Score 58; DB 2; Length 375;
Best Local Similarity 56.5%; Pred. No. 10;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 XAEAAEAARAAEAARAAEAARAA 24
DB 292 IVEGAEOAAKAAKAAEAARAA 314

RESULT 9
F90725
membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: F90725
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A/Reference number: A39629; MUID:21156331; PMID:11258796
A/Accession: F90725
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-394 <HAY>
A/Cross-references: UNIPROT:O8X965; GB:BA000007; PIDN:BAH34197.1; PID:G13360233; GSPDB:G
A/Experimental source: strain O157:H7, substrain RMD 0509552
C/Genetics:

A/Gene: EC80774

Query Match 54.3%; Score 57; DB 2; Length 394;
Best Local Similarity 56.0%; Pred. No. 14;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 1 AXAEARAAEAARAAEAARAAEAAR 25
DB 151 ADDRARAEARAAARAAARAAEA 175

RESULT 10
G85576
membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: G85576
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, E.D.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: G85576
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-394 <STO>
A/Cross-references: UNIPROT:O8X965; GB:AE005174; NID:G12513672; PIDN:AGS5075.1; GSPDB:G
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: tolA

Query Match 54.3%; Score 57; DB 2; Length 394;
Best Local Similarity 56.0%; Pred. No. 14;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 1 AXAEARAAEAARAAEAARAAEAAR 25
DB 151 ADDRARAEARAAARAAARAAEA 175

RESULT 11
T06635
hypothetical protein T20K18.120 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06635
R/Bevan, M.; Peters, S.A.; van Staveren, M.; Dikse, W.; Stiekema, W.; Bancroft, I.; New
submitted to the Protein Sequence Database, April 1999
A/Reference number: Z15790
A/Accession: T06635
A/Molecule type: DNA
A/Residues: 1-909 <BEV>
A/Cross-references: UNIPROT:Q9SU09; EMBL:AL049640; GSPDB:GN00062; ATSP:T20K18.120
A/Experimental source: cultivar Columbia; BAC clone T20K18
C/Genetics:
A/Gene: ATSP:T20K18.120
A/Map position: 4
A/Intons: 205/2; 686/3; 740/3; 772/2; 808/3; 838/3; 897/3

Query Match 54.3%; Score 57; DB 2; Length 909;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 AXAEARAAEAARAAEAARAAEAAR 21
DB 593 AHAERARAAAGAREKAEKAA 613

RESULT 12
H90909
hypothetical protein pXOI-72 - Bacillus anthracis virulence plasmid pXOI
C/Species: Bacillus anthracis
C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

C/Accession: H59099
R/Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
J. Bacteriol. 181, 6509-6515, 1999
A/Title: Sequence and organization of pXOI, the large *Bacillus anthracis* plasmid harbor
A/Reference number: A59091; MUID:99445483; PMID:10515943
A/Accession: H59099
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-101 <OK>
A/Cross-references: UNIPROT:Q9X342; GB:AF065404; NID:g4894216; PIDN:AA02376.1; PID:g489
A/Experimental source: strain Sterne
A/Note: similar to hypothetical, locus Clo tetr Clostridium perfringens (L20800)
C/Genetics:
A/Gene: pXOI-72
A/Genome: plasmid
C/Superfamily: *Bacillus anthracis* virulence plasmid pXOI hypothetical protein pXOI-72

Query Match 53.3%; Score 56; DB 2; Length 101;
Best Local Similarity 63.6%; Pred. No. 5.6;
Matches 14; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 1 AXAEAEKAKYAAAEKAKA 22
Db 44 AEEKAEEKAKAEAEKAKA 65

RESULT 13
E87612
cytochrome c, membrane-bound [imported] - *Caulobacter crescentus*
C/Species: *Caulobacter crescentus*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 15-Mar-2004
C/Accession: E87612
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Jamb, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Klot
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of *Caulobacter crescentus*.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: E87612
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-228 <STO>
A/Cross-references: GB:AE005673; NID:g13424561; PIDN:AAK24897.1; GSPDB:GN00148
C/Genetics:
A/Gene: CC2935
C/Superfamily: membrane-bound c-type cytochrome: cytochrome c homology
C/Keywords: chromoprotein; heme; iron; metalloprotein
F/81/84/Binding site: heme (Cys) (covalent) #status predicted
F/85/Binding site: heme iron (His) (axial ligand) #status predicted
F/150/Binding site: heme iron (Met) (axial ligand) #status predicted

Query Match 53.3%; Score 56; DB 2; Length 228;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Oy 1 AXAEAEKAKYAAAEKAKA 25
Db 187 APAEGAAPAAEGAAPAAEGAAPAA 211

RESULT 14
E83525
TOLa protein PA0971 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: E83525
R/Stover, C.K.; Plam, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Ba
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:1094043
A/Accession: E83525

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-347 <STO>
A/Cross-references: UNIPROT:P50600; GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AG0436C
A/Experimental source: strain PA01
C/Genetics:
A/Gene: tolA; PA0971

Query Match 53.3%; Score 56; DB 2; Length 347;
Best Local Similarity 56.0%; Pred. No. 16;
Matches 14; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 AXAEAEKAKYAAAEKAKA 25
Db 171 AKKKAADAKKKAEEKAKA 195

RESULT 15
A82152
tolA protein VC1837 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C/Species: *Vibrio cholerae*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: A82152
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A/Reference number: A82035; MUID:20406833; PMID:10952201
A/Accession: A82152
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-356 <HEI>
A/Cross-references: UNIPROT:Q9KR10; GB:AE004259; GB:AE003852; NID:g9656353; PIDN:AAF9498E
A/Experimental source: serogroup O1; strain N16961; biotype El Tor.
C/Genetics:
A/Gene: VC1837
A/Map position: 1

Query Match 53.3%; Score 56; DB 2; Length 356;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 18; Conservative 4; Mismatches 3; Indels 8; Gaps 2;

Oy 1 AXAE---AAEKAKYAAEA---EKAKA 25
Db 199 AKAEQEHLAKKAKKAKKADKAKKXKAKAKA 231

RESULT 16
AH2328
ATP-binding protein of ABC transporter all14183 [imported] - *Nostoc* sp. (strain PCC 7120)
C/Species: *Nostoc* sp. strain PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AH2328
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anat*
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AH2328
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-564 <KUR>
A/Cross-references: UNIPROT:Q8YPL1; GB:BA000019; PIDN:BA075882.1; PID:g17133318; GSPDB:GN
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: all14183
C/Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 53.3%; Score 56; DB 2; Length 564;
Best Local Similarity 61.9%; Pred. No. 25;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```
Qy      2 XAEAEKAAKYAAEAEAKA 22
      :| ||||| |::: ||
Db      542 EAIAEKAAKKAASAKSSAK 562
```

RESULT 17
IKEBCA

C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: I40784; A03504; I40777
R:Motilon, J.; Chartier, M.; Bidaud, M.; Lazdunski, C.
Mol. Gen. Genet. 211, 231-243, 1988
A:Title: The complete nucleotide sequence of the colicinogenic plasmid ColA. High extent
A:Reference number: I40778; MUID:88174422; PMID:2832701

A:Residues: 1-592 <RES>
A:Cross-references: UNIPROT:P04480; GB:M37402; PID:g144661, PID:g144667
A:Experimental source: plasmid COLA
R:Morlon, J.; Llobes, R.; Varenne, S.; Charlier, M.; Lazdunski, C.
J. Mol. Biol. 170, 221-285, 1983
A:Title: Complete nucleotide sequence of the structural gene for colicin A, a gene trans-
Reference number: A03504; MUID:84036205; PMID:6313941

A:Cross-references: GB:X01008; GB:X00034; NID:g4045; PIDN:CAA25503.1; PID:g40460
R:Morlon, J.; Llobes, R.; Chantier, M.; Bonicel, J.; Lazdunski, C.
EMBO J. 2, 787-789, 1983
A:Title: Nucleotide sequence of promoter, operator and amino-terminal region of *caa*, the
A:Reference number: I40777; MUID:84057757; PMID:6641715
A:Accession: I40777

A:Molecule type: DNA
A:Residues: 1-53, 'X', 55-70 <RE2>
A:Cross-references: GB:M6369; NID:g144659; PIDN:AA98057.1; PID:g144660
A:Experimental source: plasmid COLA
C:Comment: This protein acts to depolarize the bacterial inner membrane, most likely by
C:Genetics:
C:Gene: caa
A:Genome: plasmid
C:Superfamily: colicin IB
;Keywords: antibiotic, bacteriocin, toxin, transmembrane protein

```

Query Match 53.3% Score 56: DB 1; length 592;
      Similarity 54.2%; Pared. No. 26;
      Local 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0

```

RESULT 18
S02376
antifreeze protein precursor - yellowtail flounder
C|Species: *Limanda ferruginea* (yellowtail flounder)
C|Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C|Accession: S02376
R|Scott, G.K.; Davies, P.L.; Shears, M.A.; Fletcher, G.L.
Eur. J. Biochem. 168, 629-633, 1987
A|Title: Structural variations in the alanine-rich antifreeze proteins of the Pleuronect
A|Reference number: S02376; MUID:88029483; PMID:3665937

A:Accession number in UniProt database
A:Cross-references: UNIPROT:P09031, EMBL:X06356, NID:g6f041, PIDD:CAA29655.1, PID:g6f044
A:Note: part of this sequence, including the amino end of the mature protein, was confirmed
C:Superfamily: antifreeze protein
C:Keywords: antifreeze

F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-48/Domain: propeptide #status predicted <PRO>
F;49-96/Product: antifreeze protein #status predicted <MAT>

Query Match	52.4%	Score 55;	DB 2;	Length 97;
Best Local Similarity	56.0%	Pred. No. 7.1;		
Matches 14; Conservative	3;	Mismatches 8;	Indels 0;	Gaps 0;

Qy 1 AXAEAEKAAKYAAEAEKAAKAXA 25
| : | | | : | | | : |
Db 57 AAAATAAAAAKAAADTAAAAAKAAA 81

RESULT 19
T37490
ribosomal protein rpae - fission yeast (Schizosaccharomyces pombe)

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37490
R;Boche, G.; Pohl, T.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, November 1999
A;Reference number: Z21718

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-110 <BOT>
A:Cross-references: UNIPROT:O1317, EMBL:AL132769; PIDB:CAB59884.1; GSPDB:GN00066; SPDB:
A:Experimental source: strain 972h-, cosmid c1071
C:Genetics:
A:Gene: SPDB:SPAC1071.08
A:Map position: 1

C;Superfamily: rat acidic ribosomal protein P1

Query Match 52.4%; Score 55; DB 2; Length 110;
Best Local Similarity 60.0%; Pred. NO. 7.9;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

```

QY      1 AAEEAAEKAAKYAAEEAAEKAAKAXA 25
        | : | | | | | | | | : |
Db      70 AAAAAPPAAAGCAAPAAEEAAKEEA 94

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RESULT 20
504909 embryonic protein DC8 (clone 8/10) - carrot
CISpecies: Daucus carota (carrot)
CDate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
CAccession: 504509
R.Franz, G.; Hatzopoulos, P.; Jones, T.J.; Krauss, M.; Sung, Z.R.

A>Title: Molecular and genetic analysis of an embryonic gene, DC 8, from *Daucus carota*
A.Reference number: S04909; MUID:89384429; PMID:2571069
A.Accession: S04909
A.Status: not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 1-555 <P>
A.Cross-references: UNIPROT:P20075; GB:X16131; NID:g18333; PIDN:CM43258.2; PID:g4902466
A.Superfamily: pea seed blotin-containing protein

Query Match	52.4%	Score 55;	DB 2;	Length 555;
Best Local Similarity	52.2%	Pred. No. 32;		
Matches 12;	Conservative 5;	Mismatches 6;	Indels 0;	Gaps 0;

OY 2 XAEAAEKAKYAEEAAEKAAX 24
 :||| | : ||| :||| :
Db 195 AAEAKEKTGEYKDYAQAQKAEEAK 217

RESULT 21
151116
NF-180 - sea lamprey
C,Species: Petromyzon marinus (sea lamprey)

666; SPDB:

carota I
g4902464

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: 151116
R/Jacobs, A.J.; Kamholz, J.; Selzer, M.E.
Brain Res. Mol. Brain Res. 29, 43-52, 1995
A/Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation re
A/Reference number: 151116; MUID:95287814; PMID:7770000
A/Accession: 151116
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1110 <AC>
A/Cross-references: UNIPROT:Q91255; EMBL:U19361; NID:9632548; PIDN:AAA80106.1; PID:96325
C/Superfamily: neurofilament triplec H protein

Query Match 52.4%; Score 55; DB 2; Length 1110;
Best Local Similarity 65.0%; Pred. No. 57;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 AXAAAEKAKYAAEAEEA 20
725 AEAAEEAAKSEEAEEA 744

RESULT 22
T35781
hypothetical protein SC8A6.14c SC8A6.14c - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T35781
R/Seeger, K.J.; Harris, D.; Parkhill, J.; Bartell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A/Reference number: Z21570
A/Accession: T35781
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1147 <SE>
A/Cross-references: UNIPROT:O87848; EMBL:AL031013; PIDN:CAA19786.1; GSPDB:GN00070; SCOE
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCOE8A6.14c

Query Match 52.4%; Score 55; DB 2; Length 1147;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 12; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

1 AXAAAEKAKYAAEAEEA 24
264 AEAAAEQDVGRSAAANKARAA 287

RESULT 23
C95229
DNA-directed RNA polymerase, beta chain [imported] - Streptococcus pneumoniae (strain TI
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: C95229
R/Steitlin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Hickey, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfe,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: C95229
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1203 <KR>
A/Cross-references: UNIPROT:Q97NQ7; GB:AE005672; PIDN:AAK76028.1; PID:914973467; GSPDB:G
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SPI961
C/Superfamily: DNA-directed RNA polymerase beta chain

Query Match 51.9%; Score 54.5; DB 2; Length 1203;

Best Local Similarity 53.8%; Pred. No. 70;
Matches 14; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

1 AXAAAEKAKYAAEAEEA 25
1170 AREKAAQEAAPAEAEAKATKAA 1195

RESULT 24
G98093
DNA-directed RNA polymerase (EC 2.7.7.6) [imported] - Streptococcus pneumoniae (strain R
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: G98093
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.D.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: G98093
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1216 <KR>
A/Cross-references: UNIPROT:Q8DNF0; GB:AE007317; PIDN:AAL00580.1; PID:915459460; GSPDB:G
C/Genetics:
A/Gene: rpoB
C/Superfamily: DNA-directed RNA polymerase beta chain
C/Keywords: nucleotidyltransferase

Query Match 51.9%; Score 54.5; DB 2; Length 1216;
Best Local Similarity 53.8%; Pred. No. 70;
Matches 14; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

1 AXAAAEKAKYAAEAEEA 25
1183 AREKAAQEAAPAEAEAKATKAA 1208

RESULT 25
A26721
histone H1-gamma, embryonic - sea urchin (Strongylocentrotus purpuratus)
C/Species: Strongylocentrotus purpuratus (purple urchin)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C/Accession: A26721
R/Knowles, J.A.; Lai, Z.C.; Childs, G.J.
Mol. Cell. Biol. 7, 478-485, 1987
A/Title: Isolation, characterization, and expression of the gene encoding the late hist
A/Reference number: A26721; MUID:87172742; PMID:3031476
A/Accession: A26721
A/Molecule type: DNA
A/Residues: 1-217 <KN>
A/Cross-references: UNIPROT:P07796; GB:M16033; NID:g161517; PIDN:AAA30059.1; PID:g161518
C/Superfamily: histone H1
C/Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
F:2-217/Product: histone H1-gamma, embryonic #status predicted <MAT>

Query Match 51.4%; Score 54; DB 2; Length 217;
Best Local Similarity 54.2%; Pred. No. 18;
Matches 13; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

1 AXAAAEKAKYAAEAEEA 24
189 AAAPAKKAAKPAKAAKPAKAA 212

RESULT 26
T34809
ribosomal protein S2 - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T34809

R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z21557
A:Accession: T34809
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-310 <MOR>
A:Cross-references: UNIPROT:Q31212; EMBL:AL023797; PIDN:CAA19416.1; GSPDB:GN00070; SCOPED
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: rpbB; SCOPED:SC261.41
C:Superfamily: Escherichia coli ribosomal protein S2

Query Match 51.4%; Score 54; DB 2; Length 310;
Best Local Similarity 58.3%; Pred. No. 25;
Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 XAEEAKAKYAAEAEAKAKAXA 25
Db 261 AAEAAEAPAAEAPAAEAPAAEAPAA 304

RESULT 27
T07064
seed biotin-containing protein LEA [validated] - soybean
C:Species: Glycine max (soybean)
C:Date: 01-Sep-2000 #sequence_revision 01-Sep-2000 #text_change 09-Jul-2004
C:Accession: T07064
R;Huang, Y.C.; Tsou, C.H.; Hsu, T.F.; Chen, Z.Y.; Hsieh, K.L.; Hsieh, J.S.; Chow, T.Y.
Plant Mol. Biol. 38, 481-490, 1998
A:Title: Tissue- and stage-specific expression of a soybean (Glycine max L.) seed-mature
A:Reference number: Z15895; MUID:98416627; PMID:9747855
A:Accession: T07064
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-643 <HS1>
A:Cross-references: UNIPROT:Q39846; EMBL:U59626; NID:G1389896; PIDN:AAC61783.1; PID:G138
A:Experimental source: Strain Shi-Shi; coryledon
C:Superfamily: pea seed biotin-containing protein
C:Keywords: biotin binding; seed
F:1/5/Binding site: biotin (lys) (covalent) #status predicted

Query Match 51.4%; Score 54; DB 1; Length 643;
Best Local Similarity 52.2%; Pred. No. 47;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 XAEEAKAKYAAEAEAKAKAXA 24
Db 302 TAPVAEKAKDYLQAEEAKKAG 324

RESULT 28
T34852
probable secreted protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34852
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1999
A:Reference number: Z21559
A:Accession: T34852
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1156 <OLI>
A:Cross-references: UNIPROT:Q925A4; EMBL:AL035478; PIDN:CAB36606.1; GSPDB:GN00070; SCOPED
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC265.19

Query Match 51.4%; Score 54; DB 2; Length 1156;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 AXAEEAKAKYAAEAEAKAKAXA 24
Db 473 SAABAAKAKADSAABAAKAKADAA 496

RESULT 29
A39638
plectin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39638; S21876
R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stracowa
J. Cell Biol. 114, 83-99, 1991
A:Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with
A:Reference number: A39638; MUID:91268156; PMID:2050743
A:Accession: A39638
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-4687 <MIC>
A:Cross-references: UNIPROT:P30427; EMBL:X59601; NID:G1292885; PIDN:CAA42169.1; PID:G156
C:Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
F:6-103/Domain: ribosomal protein S10 homology <RS10>
F:184-399/Domain: alpha-actinin actin-binding domain homology <ACT>

Query Match 51.4%; Score 54; DB 1; Length 4687;
Best Local Similarity 48.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 AXAEEAKAKYAAEAEAKAKAXA 25
Db 2221 SEAAARRAAEAEAREQAEREA 2245

RESULT 30
A05163
antifreeze protein SS-8 - shorthorn sculpin
C:Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A05163
R;Hew, C.L.; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.S.
Eur. J. Biochem. 151, 167-172, 1985
A:Title: Structures of shorthorn sculpin antifreeze polypeptides.
A:Reference number: A91150; MUID:85285003; PMID:4029130
A:Accession: A05163
A:Molecule type: protein
A:Residues: 1-45 <HEW>
A:Cross-references: UNIPROT:P04368
C:Superfamily: antifreeze; blocked amino end, plasma
C:Keywords: antifreeze; blocked amino end, plasma
F:9-45/Region: alanine-rich
F:1/Modified site: blocked amino end (Met) #status experimental

Query Match 51.0%; Score 53.5; DB 2; Length 45;
Best Local Similarity 64.0%; Pred. No. 5.5;
Matches 16; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 2 XAEEAKAKYAAEAEAKAKAXA 25
Db 13 LAABAAAKRAADAAKAAKAXA 37

RESULT 31
S52418
GTP-binding regulatory protein Gs alpha-Xu chain - rat
N:Alternate names: G protein Xu-alpha-8
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 02-Feb-2001
C:Accession: S52418
R;Kehlenbach, R.H.; Matthey, J.; Hutterer, W.B.
Nature 372, 804-809, 1994
A:Title: Xu-alpha-8 is a new type of G protein.
A:Reference number: S52418; MUID:95089824; PMID:7997272

A;Accession: S52418
A;Molecule type: mRNA
A;Residues: 1-846 <KEH>
A;Cross-references: EMBL:X84047; NID:G642267; PIDN:CAAS8866.1; PID:G642268
R;Kehlenbach, R.H.; Matthey, J.; Hultner, W.B.
Nature 375, 253, 1995
A;Title: Correction: XlaIphs is a new type of G protein.
A;Reference number: S58911
A;Contents: annotation; assignment of start codon
A;Note: experimental data from this paper suggest that the translation is initiated at p
C;Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
F;132-846/Product: GTP-binding regulatory protein Gs alpha-XL chain #status experimental
F;449-506/Region: nucleotide-binding motif A (P-loop)
F;744-747/Region: GTP-binding NKXD motif

Query Match 51.0%; Score 53.5; DB 2; Length 846;
Best Local Similarity 61.5%; Pred. No. 67;
Matches 16; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 AXAEAEKAKYAAEAAEKAKAXA 25
Db 170 AAAAEEPAEPAEPAEPAEPAEPA 195

RESULT 32
FDF18G
antifreeze protein GS-8 - grubby sculpin
C;Species: Myoxocephalus aeneus (grubby sculpin)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S07046
R;Chakrabarty, A.; Hew, C.L.; Shears, M.; Fletcher, G.
Can. J. Zool. 66, 403-408, 1988
A;Title: Primary structures of the alanine-rich antifreeze polypeptides from grubby scu
A;Reference number: S06417
A;Accession: S07046
A;Molecule type: protein
A;Residues: 1-40 <CHA>
A;Cross-references: UNIPROT:P20617
C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end
F;1/Modified site: blocked amino end (Met) #status experimental

Query Match 50.5%; Score 53; DB 1; Length 40;
Best Local Similarity 58.3%; Pred. No. 5.6;
Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 XAEAEKAKYAAEAEKAKAXA 25
Db 14 AAAAALAAKTAADAAAKAAIAA 37

RESULT 33
S19114
cgr-1 protein - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S19114
R;Wakarchuk, W.W.; Mueller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
A;Title: Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements
A;Reference number: S19113; MUID:92119224; PMID:1731966
A;Accession: S19114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <MAK>
A;Cross-references: UNIPROT:Q39597; EMBL:X17207
C;Superfamily: phage lambda hypothetical protein 401

Query Match 50.5%; Score 53; DB 2; Length 205;
Best Local Similarity 52.0%; Pred. No. 23;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAEAEKAKYAAEAEKAKAXA 25

Db 124 AAAQAAAQAAERAAAQAAAQAAA 148

RESULT 34
AG0592
toIA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0592
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.W.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; S.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0592
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05209.1; PID:G16501979; GSPDB:GN00176
C;Genetics: STY0793

Query Match 50.5%; Score 53; DB 2; Length 376;
Best Local Similarity 52.0%; Pred. No. 38;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAEAEKAKYAAEAEKAKAXA 25
Db 177 AEAEEAKAAAEBAKKAEAEAKAA 201

RESULT 35
AC0138
TolA colicin import membrane protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0138
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.W.; Davis, P.; Dougan, G.; I
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrall, I
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
A;Cross-references: UNIPROT:Q8ZGZ2; GB:AL590842; PIDN:CAC09966.1; PID:G15979190; GSPDB:GN
C;Genetics: TolA

Query Match 50.5%; Score 53; DB 2; Length 388;
Best Local Similarity 59.1%; Pred. No. 39;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 BAEKAAKYAAEAEKAKAXA 25
Db 212 KAVEVAEKAADAAEKKAAADA 233

RESULT 36
T38147
dolichyl-phosphate-mannose-protein mannosyl transferase - fission yeast (Schizosaccharomy
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38147
R;Peterson, D.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21774

A:Accession: T38147
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-893 <PEA>
 A:Cross-references: UNIPROT:O1398; EMBL:Z99295; PIDN:CAB16577.1; GSPDB:GN00066; SPDB:SF
 A:Experimental source: strain 972h-; cosmid c22A12
 C:Genetics:
 A:Gene: SPDB:SPAC22A12.07C
 A:Map position: 1
 C:Superfamily: dolichyl-phosphate-mannose-protein mannosyltransferase

Query Match 50.5%; Score 53; DB 2; Length 893;
 Best Local Similarity 48.0%; Pred. No. 80;
 Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 AXAAEAERKAYAAEAERKAKAKA 25
 Db 786 AEOEAERAAERKAAERAAERSSSEA 810

RESULT 37
 H83437
 hypothetical protein PA1669 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: H83437
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: H83437
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1175 <STO>
 A:Cross-references: UNIPROT:Q91356; GB:AE004594; GB:AE004091; NID:g9947630; PIDN:AA0505
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1669

Query Match 50.0%; Score 52.5; DB 2; Length 1175;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 4; Mismatches 5; Indels 7; Gaps 1;

OY 1 AXAAEAERKAYAAEAERKAKAKA 25
 Db 802 ALAASDKAAEKCGKLGKRAAAAAGKARDALA 833

RESULT 38
 G60110
 repetitive protein antigen 69/70 - Trypanosoma cruzi (fragment)
 C:Species: Trypanosoma cruzi
 C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
 C:Accession: G60110
 R:Hoti, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blum, J.H.; Donelson, J.E.
 Infect. Immun. 57, 1959-1967, 1989
 A:Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.
 A:Reference number: A60110; MUID:8977508; PMID:2655529
 A:Accession: G60110
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-97 <HOF>
 A:Cross-references: UNIPROT:Q7M3M1
 C:Superfamily: varicella-zoster virus gene 22 protein
 C:Keywords: tandem repeat
 F11-85/Region: 7-residue repeats

Query Match 49.5%; Score 52; DB 2; Length 97;
 Best Local Similarity 56.0%; Pred. No. 16;
 Matches 14; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 AXAAEAERKAYAAEAERKAKAKA 25
 Db 51 APAKAAAAPAKTAAAPAKAAAAPA 75

RESULT 39
 D86389
 hypothetical protein P28B23.4 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: D86389
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Con, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: D86389
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-147 <STO>
 A:Cross-references: UNIPROT:Q9C674; GB:AE005172; NID:g11079518; PIDN:AA029229.1; GSPDB:G
 C:Genetics:
 A:Map position: 1

Query Match 49.5%; Score 52; DB 2; Length 147;
 Best Local Similarity 52.6%; Pred. No. 22;
 Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 2 XAAEAERKAYAAEAERKAKA 20
 Db 61 VAFTRAKSKERAAERAKA 79

RESULT 40
 T26386
 hypothetical protein Y105CSB-J - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T26386
 R:McMurray, A.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z20208
 A:Accession: T26386
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-192 <WIL>
 A:Cross-references: UNIPROT:Q9NAM6; EMBL:AL110479; NID:e1542153; PIDN:CAB54358.1; CESP:Y
 A:Experimental source: clone Y105CSB
 C:Genetics:
 A:Gene: CESP:Y105CSB-J
 A:Superfamily: human S-phase kinase-associated protein 1A

Query Match 49.5%; Score 52; DB 2; Length 192;
 Best Local Similarity 70.6%; Pred. No. 28;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 EAERKAYAAEAERKAKA 20
 Db 163 EAERAAERKAAERKAKA 179

RESULT 41
 A25550
 histone H1 - sea urchin (lytechinus pictus)
 C:Species: Lytechinus pictus (painted urchin)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A25550

R; Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A; Title: Comparison of the late H1 histone genes of the sea urchin *Lytechinus pictus* and
A; Reference number: A25550; MUID:8704078; PMID:3022245
A; Accession: A25550
A; Molecule type: DNA
A; Residues: 1-210 <KNO>
A; Cross-references: UNIPROT:P06144; GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C; Superfamily: histone H1
C; Keywords: chromosomal protein; DNA binding; nucleosome; nucleus

Query Match 49.5%; Score 52; DB 2; Length 210;
Best Local Similarity 52.0%; Pred. No. 30;
Matches 13; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 1 AXAAEAKAKYAAEAAEAKAKAXA 25
Db 179 AKKAAKAPAKKAKKAKKAPAK 203

RESULT 42

HSURP

histone H1, gonadal - sea urchin (*Parachinus angulosus*)
C; Species: *Parachinus angulosus* (angulate urchin)
C; Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 09-Jul-2004
C; Accession: A91090; A91091; A02586
R; Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B.
Eur. J. Biochem. 104, 559-566, 1980
A; Title: The primary structure of histone H1 from sperm of the sea urchin *Parachinus angulosus*
A; Reference number: A91090; MUID:80156831; PMID:6767609
A; Contents: sequence of residues 1-84
A; Accession: A91090
A; Molecule type: protein
A; Residues: 1-248 <STR>
A; Cross-references: UNIPROT:P02256
R; Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Liebold, B.
Eur. J. Biochem. 104, 567-578, 1980
A; Title: The primary structure of histone H1 from sperm of the sea urchin *Parachinus angulosus*
A; Reference number: A91091; MUID:80156832; PMID:7363905
A; Accession: A91091
A; Molecule type: protein
A; Residues: 80-248 <STR>
A; Note: 144-ArG was also found
C; Superfamily: histone H1
C; Keywords: DNA binding; nucleosome; sperm

Query Match 49.5%; Score 52; DB 1; Length 248;
Best Local Similarity 54.2%; Pred. No. 35;
Matches 13; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 2 XAAEAKAKYAAEAAEAKAKAXA 25
Db 124 KTSAAAKAKKAKAAAKAKARAKA 147

RESULT 43

S58219

ABA-inducible protein, landform-specific - *Riccia fluitans*
C; Species: *Riccia fluitans*
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C; Accession: S58219
R; Hellwege, E.M.; Dietz, K.J.; Hartung, W.
submitted to the EMBL Data Library, July 1995
A; Description: Abscisic acid causes changes in gene expression involved in the induction
A; Reference number: S58219
A; Accession: S58219
A; Molecule type: mRNA
A; Residues: 1-288 <HEL>
A; Cross-references: UNIPROT:Q41154; EMBL:X89041; NID:g929818; PIDN:CAA61439.1; PID:g9298

Query Match 49.5%; Score 52; DB 2; Length 288;
Best Local Similarity 45.8%; Pred. No. 40;

Matches 11; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
Oy 2 XAAEAKAKYAAEAAEAKAKAXA 25
Db 75 GAEEAKAEAKYGAETGAKSAAS 98

RESULT 44

S32234

transcription antitermination factor nusG - *Streptomyces griseus*
C; Species: *Streptomyces griseus*
C; Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C; Accession: S32234
R; Kuester, K.; Kuberski, S.; Piepersberg, W.; Distler, J.
submitted to the EMBL Data Library, March 1993
A; Description: Cloning and nucleotide sequence analysis of the nusG-rpL-rpL-rpL-rpL
A; Reference number: S32234
A; Accession: S32234
A; Molecule type: DNA
A; Residues: 1-294 <KUE>
A; Cross-references: UNIPROT:P36260; EMBL:X72787; NID:g57539; PIDN:CAA51296.1; PID:g60356
C; Genetics:
A; Gene: nusG
A; Start codon: GTG
A; Superfamily: transcription antitermination factor nusG
C; Keywords: transcription antitermination; transcription factor

Query Match 49.5%; Score 52; DB 2; Length 294;
Best Local Similarity 61.9%; Pred. No. 40;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 4 EAAEAKAKYAAEAAEAKAKAX 24
Db 212 EAEEKARAEAAEAGKAPAR 232

RESULT 45

S41061

probable transcription antitermination factor nusG - *Streptomyces griseus* (strain IF0133)
C; Species: *Streptomyces griseus*
A; Variety: strain IF013350
C; Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C; Accession: S41061
R; Miyake, K.; Onaka, H.; Horinouchi, S.; Beppu, T.
Biochim. Biophys. Acta 1217, 97-100, 1994
A; Title: Organization and nucleotide sequence of the secE-nusG region of *Streptomyces griseus*
A; Reference number: S41059; MUID:94114580; PMID:8286423
A; Accession: S41061
A; Molecule type: DNA
A; Residues: 1-294 <MTY>
A; Cross-references: UNIPROT:P36260; EMBL:D17464; NID:g436786; PIDN:BA04281.1; PID:g4838
A; Experimental source: strain IF013350
C; Genetics:
A; Gene: nusG
A; Start codon: GTG
C; Function:
A; Description: may be involved in antibiotics production
C; Superfamily: transcription antitermination factor nusG

Query Match 49.5%; Score 52; DB 2; Length 294;
Best Local Similarity 61.9%; Pred. No. 40;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 4 EAAEAKAKYAAEAAEAKAKAX 24
Db 212 EAEEKARAEAAEAGKAPAR 232

Search completed: July 11, 2005, 09:47:10
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2005, 09:24:04 ; Search time 167 Seconds

(without alignments)
76.659 Million cell updates/sec

Title: SEQ1
Perfect score: 105
Sequence: 1 axaeeaaekaaakaaakaxa 25

Scoring table: BIOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	67.6	485	2	Q8RXD0
2	71	67.6	924	2	Q8RXD0
3	67	63.8	278	2	Q7Q0M9
4	65	61.9	168	2	Q69907
5	63	60.0	179	1	RL19_AGR75
6	63	60.0	413	2	Q83SA1
7	63	60.0	421	1	TOLA_ECOLI
8	63	60.0	421	2	Q8FUT1
9	61	58.1	441	2	Q6N8X8
10	61	58.1	593	2	Q6N8X8
11	60.5	57.6	711	2	Q6N8X8
12	60.5	57.6	730	1	EHS_HUMAN
13	60.5	57.6	757	2	Q14234
14	60.5	57.6	757	2	Q75M03
15	60	57.1	105	2	Q6N503
16	60	57.1	177	2	Q9AB65
17	60	57.1	371	2	Q6N4V4
18	60	57.1	572	2	Q6N865
19	60	57.1	738	2	Q6UBQ3
20	60	57.1	899	2	Q6N1Z0
21	59.5	56.7	531	2	Q7PNQ9
22	59.5	56.7	547	2	Q891E4
23	59.5	56.2	347	2	Q9K1L9
24	59	56.2	389	2	Q9CM70
25	59	56.2	1020	2	Q86PC3
26	59	56.2	1020	2	Q9W2J2
27	59	56.2	1069	2	Q86BG1
28	58.5	55.7	181	2	Q64SR3
29	58.5	55.7	496	2	Q8VQW6
30	58.5	55.7	508	2	Q9VGD2
31	58.5	55.7	664	2	Q9VGD3

32	58.5	55.7	694	2	Q8SWT7
33	58.5	55.7	1171	2	Q9P3E2
34	58	55.2	92	2	Q9DF23
35	58	55.2	124	2	Q7V6K8
36	58	55.2	387	2	Q96113
37	58	55.2	358	2	Q7RW57
38	58	55.2	575	2	Q6PF71
39	58	55.2	660	2	Q88YV9
40	58	55.2	809	2	P90534
41	58	55.2	2197	1	P0L1_TORVR
42	57.5	54.8	638	2	Q891E3
43	57	54.3	190	2	Q15860
44	57	54.3	394	2	Q8X965
45	57	54.3	508	2	Q875A8

ALIGNMENTS

RESULT 1	ID	Q8RXD0	PRELIMINARY;	PRT;	485 AA.
DT	01-JUN-2002	(TREMblrel. 21, Created)			
DT	01-JUN-2002	(TREMblrel. 21, Last sequence update)			
DT	05-JUN-2004	(TREMblrel. 27, Last annotation update)			
DE	Auxilin-like protein (At4g12780).				
GN	Name=At4g12780;				
OC	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.				
OK	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,				
RA	Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,				
RA	Chen R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,				
RA	Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,				
RA	Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,				
RA	Ecker J., Theologis A., Davis R.W.,				
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Shim P., Chen H., Chen R., Kim C.J., Bowser L., Carninci P.,				
RA	Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,				
RA	Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,				
RA	Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,				
RA	Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,				
RA	Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,				
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY081334; ALU91223.1; -				
DR	EMBL; BT009679; AAP81797.1; -				
DR	HSSP; Q27974; INZ6				
DR	InterPro; IPR001623; DnaU_N.				
DR	SMART; SM00271; DnaU; 1.				
SQ	SEQUENCE 485 AA; 54793 MW; 1054AD1021DB52AD5 CRC64;				
Query Match	67.6%; Score 71; DB 2; Length 485;				
Best Local Similarity	68.0%; Pred. No. 2.1;				
Matches	17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;				
QY	1 AXAEEAAKAAKAAKAAKAAKAA 25				
DB	184 AAAGARDKAAKAAKAAKAAKAA 208				
RESULT 2					
Q9SU08	PRELIMINARY;				
ID	Q9SU08	PRT;	924 AA.		
AC	Q9SU08;				
DT	01-MAY-2000 (TREMblrel. 13, Created)				
DT	01-MAY-2000 (TREMblrel. 13, Last sequence update)				

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DT 05-JUN-2004 (TReMBLrel. 27, last annotation update)
DE Auxilin-like protein.
GN Name=T20X18.130; Synonyms=AT4g12780;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCB1_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
RA Bancroft I., Mewes H.W., Mayer K.F.X., Scheller C.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL0496640; CAB40995.1; -.
DR EMBL; AL161534; CAB78320.1; -.
DR PIR; T06636; T06636.
DR HSSP; Q27974; INZ6.
DR InterPro; IPR001623; DnaJ_N.
DR SMART; SM00271; DnaJ_1.
SQ SEQUENCE 924 AA; 102223 MW; 26E22C7C831EFF9B CRC64;

Query Match 67.6%; Score 71; DB 2; Length 924;
Best Local Similarity 68.0%; Pred. No. 3.5;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 AXAAEAERKAKYAAEAERKAKAXA 25
Db 603 AAAGARDKAAKAAAEAREKAKAA 627

RESULT 3
O7Q0M9 PRELIMINARY; PRT; 278 AA.
AC O7Q0M9;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE AGCP8317 (Fragment).
GN Name=agCG54338; ORFNames=ENSAAG0000011932;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCB1_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=PEST;
RA Anophles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein L13p family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008980; EA114246.1; -.
DR HSSP; O59300; I33A.
DR GO; GO:0015934; C:large ribosomal subunit; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR005822; Ribosomal_L13.
DR InterPro; IPR005755; Ribosomal_L13e/a.
DR Pfam; PF00572; Ribosomal_L13; 1.

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DR ProDom; PD001791; Ribosomal_L13; 1.
DR TIGRFAMs; TIGR01077; L13_A_E; 1.
DR PROSITE; PS00783; RIBOSOMAL_L13; 1.
KM Ribonucleoprotein; Ribosomal protein.
FT NON RPR
SQ SEQUENCE 278 AA; 31601 MW; D47C71B78A302495 CRC64;

Query Match 63.8%; Score 67; DB 2; Length 278;
Best Local Similarity 65.2%; Pred. No. 3.8;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 XAEEAEKAKYAAEAERKAKAX 24
Db 243 AAARAEKAKYAAEAERKAKAT 265

RESULT 4
O69907 PRELIMINARY; PRT; 168 AA.
AC O69907;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, last annotation update)
DE Hypothetical protein SC05619.
GN ORFNames=SC2EL.36;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCB1_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; Pubmed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wierczek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL39124; CA119411.1; -.
DR PIR; T34804; T34804.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 168 AA; 17934 MW; 72063B195040BD6E CRC64;

Query Match 61.9%; Score 65; DB 2; Length 168;
Best Local Similarity 62.5%; Pred. No. 4.4;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 AXAAEAERKAKYAAEAERKAKAX 24
Db 106 AEAARAEKAKYAAEAERKAKAP 129

RESULT 5
RL19_AGR75 STANDARD; PRT; 179 AA.
ID RL19_AGR75;
AC O8UBZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE 508 ribosomal protein L19.
GN Name=rpL5; Ordered locus names=Atu2703, AGR C 4900;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCB1_TaxID=176299;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. St.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kuyavayn T., Levy R., Li M.-J., McClelland B., Palmieri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neeter E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
CS8."
RL Science 294:2317-2323 (2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Outollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens CS8."
RL Science 294:2323-2328 (2001).
CC -1- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminocycl-tryna binding site (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein L19 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE009216; AAL43684.1; -
DR EMBL; AE008183; AAK8423.1; -
DR PIR; AF2908; AF2908.
DR PIR; P97683; P97683.
DR HAMAP; MF_00402; -; 1.
DR InterPro; IPR001857; Ribosomal_L19.
DR Pfam; PF01245; Ribosomal_L19; 1.
DR PRINTS; PR00061; RIBOSOMAL_L19.
DR PRODOM; PD002979; Ribosomal_L19; 1.
DR TIGRfam; TIGR01024; rplS_bact; 1.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
RW Complete proteome; Ribosomal protein.
SQ SEQUENCE 179 AA; 19474 MW; F356BA44A5AD2D1 CRC64;

Query Match 60.0%; Score 63; DB 1; Length 179;
Best Local Similarity 69.2%; Pred. No. 7.8;
Matches 18; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

OY 1 AXAEMAKAKYAAE--AAEKAKAX 24
DB 149 AQAALAEKAAEAARAAAEKAAAEKAA 174

RESULT 6
O83SA1 PRELIMINARY; PRT; 413 AA.
AC O83SA1: OTC204;
DT 01-UN-2003 (TIGRfamrel. 24, Created)
DT 01-UN-2003 (TIGRfamrel. 24, Last sequence update)
DT 25-OCT-2004 (TIGRfamrel. 28, Last annotation update)
DE Membrane spanning protein, required for outer membrane integrity.
GN Name=tolA; OrderedLocustNames=S0571, S0558;
OS Shigella flexneri.

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=301 / Serotype 2a;
RX MEDLINE=22274406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441 (2002).
[2]
RP SEQUENCE FROM N.A.
RX STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Maynew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RL Infect. Immun. 71:2775-2786 (2003).
DR EMBL; AE015086; AAK42202.1; -
DR EMBL; AE016979; AAP16075.1; -
DR HSSP; P19934; ITOL.
DR InterPro; IPR010528; TolA.
DR Pfam; PF06519; TolA; 1.
RW Complete proteome.
SQ SEQUENCE 413 AA; 4235 MW; 93E10F2C5DE0D8 CRC64;

Query Match 60.0%; Score 63; DB 2; Length 413;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 15; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 AXAEMAKAKYAAEAAAEKAKAXA 25
DB 143 ADARAAEAERAAADAKKAAEA 167

RESULT 7
ID TOL-ECOLI STANDARD; PRT; 421 AA.
AC P19934;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE TolA protein.
GN Name=tolA; Synonyms=clm, excC, lky; OrderedLocustNames=b0739;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / JMI05;
RX MEDLINE=90078104; PubMed=2687247;
RA Levengood S.K., Webster R.B.;
RT "Nucleotide sequences of the tolA and tolB genes and localization of
RT their products, components of a multistep translocation system in
RT Escherichia coli."
RL J. Bacteriol. 171:6600-6609 (1989).
[2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=9742617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

```

RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN:K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizubuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Samped G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiiuchi T.;
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 RN [4]
 RP DOMAINS.
 RX MEDLINE=91296736; PubMed=2068069;
 RA Levengood S.K., Beyer W.F. Jr., Webster R.E.;
 RT "TolA: a membrane protein involved in colicin uptake contains an
 extended helical region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
 RN [5]
 RP INTERACTION WITH PORINS.
 RX MEDLINE=97133271; PubMed=8978668;
 RA Derouiche R., Gavioji M., Benedetti H., Prilipov A., Lazdunski C.,
 RA Llobes R.;
 RT "TolA central domain interacts with *Escherichia coli* porins.";
 RL BMO J. 15:6408-6415(1996).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.
 RX MEDLINE=99332679; PubMed=10404600; DOI=10.1016/S0969-2126(99)80092-6;
 RA Lubkoweki J., Henneke F., Plueckhuhn A., Wlodawer A.;
 RT "Filamentous phage infection: crystal structure of gfp in complex with
 its coreceptor, the C-terminal domain of TolA.";
 RL Structure 7:711-722(1999).
 CC -1- FUNCTION: Involved in the tonB-independent uptake of group A
 colicins (colicins A, E1, E2, E3, and K). Necessary for the
 colicins to reach their respective targets after initial binding
 to the bacteria. Also involved in the translocation of
 bacteriophage DNA.
 CC -1- SUBUNIT: Interacts, via domain II, with porins ompC, phoE and
 lamb.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
 CC -----
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 CC -----
 CC EMBL; M28232; AAA24683.1; -
 DR EMBL; U00096; AAC73833.1; -
 DR EMBL; D90713; BAA35405.1; -
 DR PIR; JY0057; JY0057.
 DR PDB; 1TOL; X-ray; A--
 DR ECHOBASE; EB1000; -
 DR EcoGene; EG1007; TOLa.
 DR InterPro; IPR010528; TOLa.
 DR Pfam; PF06519; TOLa; 1.
 KW 3D-structure; Bacteriophage; Complete proteome;
 KW Inner membrane; Protein transport; Repeat; Transmembrane; Transport.
 FT DOMAIN 1 13 Cytoplasmic (Potential).
 FT TRANSMEM 14 34 Potential.
 FT DOMAIN 35 421 Periplasmic (Potential).
 FT DOMAIN 48 310 Domain II (alpha-helical).
 FT DOMAIN 311 421 Domain III (functional).
 FT DOMAIN 224 292 13 X tandem repeats of [EDA]-K(1,2)-
 FT REPEAT 224 229 1.(2,4).
 FT REPEAT

FT REPEAT 230 234 2.
 FT REPEAT 235 240 3.
 FT REPEAT 241 245 4.
 FT REPEAT 246 250 5.
 FT REPEAT 251 255 6.
 FT REPEAT 256 260 7.
 FT REPEAT 261 266 8.
 FT REPEAT 267 271 9.
 FT REPEAT 272 277 10.
 FT REPEAT 278 282 11.
 FT REPEAT 283 287 12.
 FT REPEAT 288 292 13.
 FT DISULFID 363 388
 FT HELIX 335 349
 FT TURN 350 351
 FT TURN 353 354
 FT HELIX 355 358
 FT TURN 359 360
 FT STRAND 363 369
 FT TURN 371 372
 FT STRAND 375 383
 FT HELIX 385 397
 FT HELIX 406 412
 FT TURN 413 414
 FT STRAND 416 421
 SQ SEQUENCE 421 AA; 43156 MW; 8B2F52B4B97C655E CRC64;
 Query Match 60.0%; Score 63; DB 1; Length 421;
 Best Local Similarity 60.0%; Pred. No. 16;
 Matches 15; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 AXAAEAERAKKAYAAEAERAKAKAXA 25
 Db 151 ADAKAAEAERAKKAAADAKKAAEA 175
 RESULT 8
 ID 08FUT1 PRELIMINARY; PRT; 421 AA.
 AC 08FUT1;
 DT 01-MAR-2003 (TREMURel. 23, Created)
 DT 01-MAR-2003 (TREMURel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMURel. 26, Last annotation update)
 DE TolA protein.
 GN Name:TolA; OrderedLocNames=c0818;
 OS *Escherichia coli* O6
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:O6:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22386234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raebou D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Domeneberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AE016757; AAN79291.1; -
 DR HSSP; P19934; 1TOL.
 DR InterPro; IPR010528; TOLa.
 DR Pfam; PF06519; TOLa; 1.
 KW Complete proteome.
 SQ SEQUENCE 421 AA; 43184 MW; DB296626F056D385 CRC64;
 Query Match 60.0%; Score 63; DB 2; Length 421;
 Best Local Similarity 60.0%; Pred. No. 16;
 Matches 15; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 AXAAEAERAKKAYAAEAERAKAKAXA 25

Db 151 ADAKAAEAAKAAADAKKAAEA 175

RESULT 9

Q6N8X8 PRELIMINARY; PRT; 441 AA.

AC Q6N8X8; 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE OmpA/MotB domain, possible porin precursor.

GN OrderedLocustNames=RP11774;

OS Rhodopseudomonas palustris.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Rhodopseudomonas.

OX NCBI_TaxID=1076;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CGA009 / ATCC BAA-98;

RX PubMed=14704707; DOI=10.1038/nbt923;

RA Latimer P.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pellecier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobet C., Torres Y Torres J.L., Peters C., Harrison F.H., Gibson J., Harwood C.S.;

RT "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";

RL Nat. Biotechnol. 22:55-61(2004).

CC -1- SIMILARITY: Belongs to the ompA family.

DR EMBL: BX572598; CAZ7215.1; -

DR GO: GO:0016021; C:Integral to membrane; IEA.

DR GO: GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.

DR GO: GO:0015288; F:porin activity; IEA.

DR InterPro: IPR006664; Bac_OmpA.

DR InterPro: IPR006665; OmpA/MotB.

DR Pfam: PF00691; OmpA; 1.

DR PRINTS: PRO1021; OMPADOMAIN.

DR ProDom: PD000930; OmpA/MotB; 1.

KM Complete proteome; Porin; Signal.

FT SIGNAL 1 27 Potential.

ST SEQUENCE 441 AA; 44811 MW; F6B866A4FE183A0 CRC64;

SO

Query Match 58.1%; Score 61; DB 2; Length 441;

Best Local Similarity 62.5%; Pred. No. 28;

Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAAEAAKAAKAAEAAKAAKAX 24

Db 237 ADSEAKAAKAAKAAEAAKAAK 260

RESULT 10

Q8ZNE5 PRELIMINARY; PRT; 593 AA.

AC Q8ZNE5; 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE Putative von Willebrand factor, vWF type A domain.

GN Name=vFbk; OrderedLocustNames=STM2315;

OS Salmonella typhimurium;

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2;

RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

RA McClelland M., Sanderson K.E., Speeth J., Clifton S.W., Lacroille P., Courtney L., Poroylik S., Ali J., Dante M., Du P., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

RT LT2.";

RL Nature 413:852-856(2001).

DR EMBL: AF008803; AAL21216.1; -

DR Pfam: PF00092; VWA; 1.

DR SMART: SM00327; VWA; 1.

DR PROSITE: PS50234; VWFA; 1.

SO SEQUENCE 593 AA; 64640 MW; 595CA8158968357 CRC64;

Qy 2 XAAEAAKAAKAAEAAKAAKAXA 25

Db 57 QAEEAQAQAAKAAEAAKAAKALADA 80

RESULT 11

Q7Z3F5 PRELIMINARY; PRT; 711 AA.

AC Q7Z3F5; 01-OCT-2003 (TREMBlrel. 25, Created)

DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DE Hypothetical protein DKFZp686f06102.

GN Name=DKFZp686f06102;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Human fetal kidney;

RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: BX57939; CAD97910.1; -

DR InterPro: IPR01451; Hexapep_transf.

DR PROSITE: PS00101; HEXAPEP_TRANSFERSASES; UNKNOWN_1.

KM Hypothetical protein.

ST SEQUENCE 711 AA; 61765 MW; 95B624A9BA89B CRC64;

SO

Query Match 57.6%; Score 60.5; DB 2; Length 711;

Best Local Similarity 58.6%; Pred. No. 47;

Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

Qy 1 AXAAEAAKAAK-----AAEAAKAAKAX 24

Db 446 AQAAPAAKAAKAGVTPAAAPAAKAAKAXA 474

RESULT 12

ELS_HUMAN STANDARD; PRT; 730 AA.

AC P15502; Q14233; Q14238;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DE 25-OCT-2004 (Rel. 45, Last annotation update)

GN Elastin precursor (Tropoelastin).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM B).

RC MEDLINE=87289666; PubMed=3039501;

RX Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N., Rosenbloom J.C., Peltonen L., Rosenbloom J.;

RT "Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA.";

RT Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).

RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=89090960; PubMed=3171221;
 RA Fazio M.J., Olsen D.R., Kaub E.A., Baldwin C.T., Indik Z.,
 RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;
 RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
 RT recombinant cDNA library: further elucidation of alternative splicing
 RT utilizing exon-specific oligonucleotides."
 RL J. Invest. Dermatol. 91:458-464(1988).
 RN [3]
 RP SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
 RC TISSUE=Placenta;
 RX MEDLINE=88156133; PubMed=2831431;
 RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
 RA Rosenbloom J., Uitto J.;
 RT "Isolation and characterization of human elastin cDNAs, and age-
 RT associated variation in elastin gene expression in cultured skin
 RT fibroblasts."
 RL Lab. Invest. 58:270-277(1988).
 RN [4]
 RP SEQUENCE OF 603-730 FROM N.A.
 RC TISSUE=Hipocampus, and Placenta;
 RX MEDLINE=96291399; PubMed=8689688; DOI=10.1016/S0092-8674(00)80077-X;
 RA Frangiskakis J.M., Swart A.K., Morris C.A., Mervin C.B., Bertrand J.,
 RA Robinson B.F., Klein B.P., Emery L.A., Green E.D.,
 RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.D.,
 RA Keating M.T.;
 RT "Lim-kinase1 hemizyosity implicated in impaired visuospatial
 RT constructive cognition."
 RL Cell 86:59-69(1996).
 RN [5]
 RP INVOLVEMENT IN CUTIS LAXA.
 RX MEDLINE=99091639; PubMed=9873040; DOI=10.1074/jbc.274.2.981;
 RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
 RT "Cutis laxa arising from frameshift mutations in exon 30 of the
 RT elastin gene (ELN)."
 RL J. Biol. Chem. 274:981-986(1999).
 RN [6]
 RP INVOLVEMENT IN SVAS.
 RX PubMed=10942104.
 RA Urban Z., Michals V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
 RA Munnich A., Syskens B., Gwilling M., Devriendt K., Boyd C.D.;
 RT "Isolated supravalvular aortic stenosis: functional haploinsufficiency
 RT of the elastin gene as a result of nonsense-mediated decay."
 RL Hum. Genet. 106:577-588(2000).
 CC -1- FUNCTION: Major structural protein of tissues such as aorta and
 CC nuchal ligament, which must expand rapidly and recover completely.
 CC -1- SUBUNIT: The polymeric elastin chains are cross-linked together
 CC into an extensible 3D network.
 CC -1- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P15502-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P15502-2; Sequence=VSP_004243;
 CC -1- PTM: The crosslinks are made of deaminated lys.
 CC -1- DISEASE: Defects in ELN are a cause of autosomal dominant cutis
 CC laxa [MIM:13700]. Cutis laxa is a rare connective tissue disorder
 CC characterized by loose, hyperextensible skin with decreased
 CC resilience and elasticity leading to a premature aged appearance.
 CC The skin changes are often accompanied by extracutaneous
 CC manifestations, including pulmonary emphysema, bladder
 CC diverticula, pulmonary artery stenosis and pyloric stenosis.
 CC -1- DISEASE: Haploinsufficiency of ELN may be the cause of certain
 CC cardiovascular and musculo-skeletal abnormalities observed in
 CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare
 CC developmental disorder and a contiguous gene deletion syndrome
 CC involving genes from chromosome band 7q11.23.
 CC -1- DISEASE: Defects in ELN are the cause of supravalvular aortic
 CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of

CC the ascending aorta which can occur sporadically, as an autosomal
 CC dominant condition, or as one component of Williams-Beuren
 CC syndrome.
 CC -----
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 CC -----
 CC EMBL; M17282; AAC98394.1; -.
 CC EMBL; M16983; AAC98394.1; JOINED.
 CC EMBL; M17265; AAC98394.1; JOINED.
 CC EMBL; M17266; AAC98394.1; JOINED.
 CC EMBL; M17267; AAC98394.1; JOINED.
 CC EMBL; M17268; AAC98394.1; JOINED.
 CC EMBL; M17270; AAC98394.1; JOINED.
 CC EMBL; M17271; AAC98394.1; JOINED.
 CC EMBL; M17272; AAC98394.1; JOINED.
 CC EMBL; M17273; AAC98394.1; JOINED.
 CC EMBL; M17275; AAC98394.1; JOINED.
 CC EMBL; M17276; AAC98394.1; JOINED.
 CC EMBL; M17277; AAC98394.1; JOINED.
 CC EMBL; M17278; AAC98394.1; JOINED.
 CC EMBL; M17279; AAC98394.1; JOINED.
 CC EMBL; M17280; AAC98394.1; JOINED.
 CC EMBL; M17281; AAC98394.1; JOINED.
 CC EMBL; M36860; AA52382.1; -.
 CC EMBL; M24782; AA53190.1; -.
 CC EMBL; U62292; AAB17544.1; -.
 CC EMBL; X15603; CA333627.1; -.
 CC PIR; A32707; EAHU.
 CC HSP; P50099; 1ZRF.
 CC Gene; HGNC:3327; ELN.
 CC MIM; 130160; -.
 CC MIM; 123700; -.
 CC MIM; 194050; -.
 CC MIM; 185500; -.
 CC GO; GO:0005578; C:extracellular matrix; TAS.
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 CC GO; GO:0008283; P:cell proliferation; TAS.
 CC GO; GO:0008015; P:circulation; TAS.
 CC GO; GO:0009887; P:organogenesis; TAS.
 CC GO; GO:0007585; P:respiratory gaseous exchange; TAS.
 CC InterPro; IPR003978; Tropoelastin.
 CC PRINTS; PR01500; TROPOLASTIN.
 CC KX Alternative splicing; Repeat; Signal; Structural protein;
 CC Williams-Beuren syndrome.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 730 Elastin.
 CC FT DISULFID 720 725 By similarity.
 CC FT VARSPPLIC 472 477 Missing (in isoform 2).
 CC FT /FTId=VSP_004243.
 CC SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;
 CC
 CC Query Match 57.6%; Score 60.5; DB 1; Length 730;
 CC Best Local Similarity 58.6%; Pred. No. 48;
 CC Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;
 CC
 CC Oy 1 AXAAAEKAKY-----AAAEKAKAX 24
 CC Db 441 AQAATAAKAKYGVTPAATAAKAKAXA 469
 CC
 CC RESULT 13
 CC ID 014234 PRELIMINARY; PRT; 757 AA.
 CC AC 014234;
 CC DT 01-NOV-1996 (TREMBlrel. 01, Created)
 CC DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)

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DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Elastin.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RA "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicilia G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RA "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
DR EMBL; M16983; AAC98395.1; JOINED.
DR EMBL; M17265; AAC98395.1; JOINED.
DR EMBL; M17266; AAC98395.1; JOINED.
DR EMBL; M17267; AAC98395.1; JOINED.
DR EMBL; M17268; AAC98395.1; JOINED.
DR EMBL; M17270; AAC98395.1; JOINED.
DR EMBL; M17271; AAC98395.1; JOINED.
DR EMBL; M17272; AAC98395.1; JOINED.
DR EMBL; M17273; AAC98395.1; JOINED.
DR EMBL; M17274; AAC98395.1; JOINED.
DR EMBL; M17275; AAC98395.1; JOINED.
DR EMBL; M17276; AAC98395.1; JOINED.
DR EMBL; M17277; AAC98395.1; JOINED.
DR EMBL; M17278; AAC98395.1; JOINED.
DR EMBL; M17279; AAC98395.1; JOINED.
DR EMBL; M17280; AAC98395.1; JOINED.
DR EMBL; M17281; AAC98395.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); NAS.
DR GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 757 AA; 66136 MW; 2387F55B8AF5C86 CRC64;

Query Match 57.6%; Score 60.5; DB 2; Length 757;
Best Local Similarity 58.6%; Pred. No. 49;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

OY 1 AXAEEAEKAKY-----AAEAERAKAKX 24
Db 441 AAAAAAAAAAKKYGCTPAAAAAKAAKAA 469

RESULT 14
O75MUS PRELIMINARY; PRT; 757 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein ELN.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., Olafsson M.D., Schaller M.E.,
RA Fowell J.A., Delahunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Birdsall-Corrum H., Ali J., Andrews S., Isak A.,
RA Vandrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Hartins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.M.,
RA Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.M., Abbott A., Mink P., Maupin R., Strommat C.,
RA Latreille P., Miller N., Johnson D., Murray J., Weissen J.P.,
RA Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spiehl J.,
RA Bieri J.A., Nelson J.O., Berkowicz N., Wohldmann P.B., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flieck P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005056; AAS07435.1; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005578; C:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 757 AA; 66106 MW; 2824F955D8360738 CRC64;

Query Match 57.6%; Score 60.5; DB 2; Length 757;
Best Local Similarity 58.6%; Pred. No. 49;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

OY 1 AXAEEAEKAKY-----AAEAERAKAKX 24
Db 441 AAAAAAAAAAKKYGCTPAAAAAKAAKAA 469

RESULT 15
O6N503 PRELIMINARY; PRT; 105 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=RP33180;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiales; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RA PubMed=14704707; DOI=10.1038/nbt923;
RA Latimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobat C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile

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RT photosynthetic bacterium Rhodospseudomonas palustris.",
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572603; CAE28621.1; -.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; F:nucleosome assembly; IEA.
DR InterPro; IPR005819; Histone_H5.
DR PRINTS; PR00624; HISTONEH5.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 105 AA; 11042 MW; CEBB59B3D937E980 CRC64;

Query Match 57.1%; Score 60; DB 2; Length 105;
Best Local Similarity 56.0%; Pred. No. 11;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AXAEAAEKAAKYAAEAEEKAAXA 25
Db 58 AAKTAAKAAKAAKAPKAAKAAKAA 82

RESULT 16
ID Q9AB65 PRELIMINARY; PRT; 177 AA.
AC Q9AB65;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE ATP synthase F0, B' subunit.
GN OrderedLocusNames=CC0366;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nielsen W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R., Ohta N., Maddock J.R.,
RA Porocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Dirkin A.S., Gwinn M.L., Haft D.H.,
RA Kolony J.F., Smt J., Craven M.B., Knouri H.M., Shetty J.,
RA Berry K.J., Ulteback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- SIMILARITY: Belongs to the ATPase B chain family.
DR EMBL; AE005710; AAK2353.1; -.
DR PIR; E87294; E87294.
DR TIGR; CC0366; -.
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0015078; F:hydrogen ion transporter activity; IEA.
DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.
DR GO; GO:0015986; P:ATP synthase coupled proton transport; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002146; ATPsyn B/B' sub.
DR Pfam; PF00430; ATP-syn_B_1.
DR CF(0); Complete proteome; Hydrogen ion transport; Ion transport;
KM Transmembrane; Transport.
SQ SEQUENCE 177 AA; 18465 MW; 6F0A2B32CC3D2912 CRC64;

Query Match 57.1%; Score 60; DB 2; Length 177;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AXAEAAEKAAKYAAEAEEKAAXA 25
Db 110 ASAEAAERQAQAEAVLAEKLAAEA 134

RESULT 17

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Q6N4V4
ID Q6N4V4 PRELIMINARY; PRT; 371 AA.
AC Q6N4V4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3).
GN Name=adk; OrderedLocusNames=RPB3229;
OS Rhodospseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodospseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tdbica P.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Pires C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RA "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodospseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
CC -1- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
DR EMBL; BX572603; CAE28670.1; -.
DR HSSP; P05082; IAKE.
DR GO; GO:0004017; F:adenylate kinase activity; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000850; Adenylate_kin.
DR InterPro; IPR06259; Adenyl_kin_sub.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKINASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KM ATP-binding; Complete proteome; Kinase; Transferase.
SQ SEQUENCE 371 AA; 37905 MW; 9BB86A147A346206 CRC64;

Query Match 57.1%; Score 60; DB 2; Length 371;
Best Local Similarity 56.0%; Pred. No. 32;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AXAEAAEKAAKYAAEAEEKAAXA 25
Db 306 AAKAKKKAAKAAKAAKAAKAAKAAKAA 330

RESULT 18
ID Q6N4V4 PRELIMINARY; PRT; 572 AA.
AC Q6N4V4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative invasion protein.
GN OrderedLocusNames=DIP1281;
OS Corynebacterium diptheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Blot type gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gk9874;
RA Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
RA Pallen M.J., Bentley S.D., Beara G.S., Churcher C.M., James K.D.,

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RA Celniker S.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 SH3 domain.
DR EMBL; BT003215; AAO24970.1; -
DR HSPSP; P06241; 1SHF.
DR FLYBase; FBgn0034606; CG18375.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00023; Ank; 2.
DR Pfam; PF00018; SH3_1; 1.
DR PRINTS; PR01415; ANKRYIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SMO0248; ANK; 2.
DR SMART; SMO0326; SH3; 1.
DR PROSITE; PS50088; ANK_REPEAT; 2.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50002; SH3; 1.
KW ANK repeat; SH3 domain.
SQ
SEQUENCE 1020 AA; 110433 MW; 42A3AE30EC71787B CRC64;

Query Match 56.2%; Score 59; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 93;
Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy 1 AXAEAEKAKYAAAEKAKAXA 25
Db 462 AAAAAAAAAAQAAMAEANQATTA 486

RESULT 26
OQ9W2J2 PRELIMINARY; PRT; 1020 AA.
ID OQ9W2J2
AC OQ9W2J2
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE CG18375-PA.
GN ORFNames=CG18375.
OS Drosophila melanogaster (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

[1]
SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil W.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabot G.L.,
RA Abell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes N., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz S., Ferrier W.M., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalaali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liao X., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).

[2]
SEQUENCE FROM N.A.
RA MEDLINE=2242605; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RL melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[3]
SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RL a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

[4]
SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

[5]
SEQUENCE FROM N.A.
RX Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN (6)
RP SEQUENCE FROM N.A.
RG FLYBase;
RA FLYBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 SH3 domain.
DR EMBL; AB003453; AAP46699.3; -
DR HSPSP; P06241; 1SHF.
DR InterPro; IPR002110; ANK.
DR FLYBase; FBgn0034606; CG18375.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00023; Ank; 2.
DR PRINTS; PR01415; ANKRYIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SMO0248; ANK; 2.
DR SMART; SMO0326; SH3; 1.
DR PROSITE; PS50088; ANK_REPEAT; 2.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50002; SH3; 1.
KW ANK repeat; SH3 domain.
SQ
SEQUENCE 1020 AA; 110374 MW; B18C928C514333DC CRC64;

Query Match 56.2%; Score 59; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 93;

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Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Cy 1 AXAEAEKAKYAAAEAEKAKAXA 25
Db 462 AAAAAAAAAAQAEEAANQATATAA 486

RESULT 27
086BG1 PRELIMINARY; PRT; 1069 AA.
AC 086BG1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG18375-PB.
GN ORENAMEs=CG18375;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132, DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baker E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bockova D., Bolchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.U., Wei M.H., Ibegam C.,
RA Jaisli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rehnert K., Remington K., Saunders R.D., Scheefer F., Shen H.,
RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence."

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RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatic
genome perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminler J.S., Milburn G.H., Prochman S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betancourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RP SEQUENCE FROM N.A.
RX FLYbase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FLYbase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 SH3 domain.
DR EMBL; AE003453; AF041341.1; -.
DR HSSP; P06241; 1SHF.
DR FLYbase; FBgn0034606; CG18375.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00023; Ank; 2.
DR Pfam; PF00018; SH3 1; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRODOM; PD000066; SH3; 1.
DR SMART; SM00248; ANK; 2.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PSS0088; ANK_REPEAT; 2.
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PSS0002; SH3; 1.
KV ANK repeat; SH3 domain.
SQ SEQUENCE 1069 AA; 11518 MW; BF102B0C044F80DA CRC64;

Query Match 56.2%; Score 59; DB 2; Length 1069;
Best Local Similarity 60.0%; Pred. No. 97;
Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Cy 1 AXAEAEKAKYAAAEAEKAKAXA 25
Db 511 AAAAAAAAAAQAEEAANQATATAA 535

RESULT 28
064SR3 PRELIMINARY; PRT; 181 AA.
AC 064SR3;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE 30S ribosomal protein S16.
GN ORENAMEs=BF2716;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=YCH46;
RA Kuvshara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuvshara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT insertions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
RW EMBL; AP006841; BAD9466.1; -.
KW Ribosomal protein.
SQ SEQUENCE 181 AA; 19609 MW; 3583BF4EC4DCAD3 CRC64;

Query Match
Best Local Similarity 64.0%; Pred. No. 26;
Matches 16; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Oy 1 AXAAAEKAAKAAEA-AEKAAKAX 24
Db 148 AEKAAAEKAAKAAEA-AEKAAKAX 172

RESULT 29
O8VQW6 PRELIMINARY; PRT; 496 AA.
AC O8VQW6;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Rnfc.
GN Name=rnfC;
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RA Rubio L.M., Brown C.S., Ludden P.W.;
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF450501; AAL47174.1; -.
DR HSSP; Q45560; LBWE.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR Pfam; PF01512; Complex1_5IK; 1.
DR Pfam; PF00037; Per4; 2.
DR TIGRFAMs; TIGR01945; rnfC; 1.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW 4Fe-4S; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 496 AA; 52171 MW; 0F153E1B83A10E5B CRC64;

Query Match
Best Local Similarity 55.7%; Score 58.5; DB 2; Length 496;
Matches 16; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

Oy 2 XABAABKAAKAAEA-AEKAAKAXA 25
Db 465 AAKAAAKAAKAAEA-AEKAAKAXA 487

RESULT 30
O9VGD2 PRELIMINARY; PRT; 508 AA.
AC O9VGD2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE CG31361-PB.
GN ORFNames=CG31361;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer J.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abill J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolashikov S.,
RA Botkova D., Botchan M.R., Boulter J., Brockstein P., Brotlier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertey J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.V., Wei M.H., Ibegyan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Part V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheefel F., Shen H.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodeger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195 (2000).

[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).

[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celinker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).

[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.W., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";

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RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB003694; AAF54751.2; -
DR FlyBase; FBgn0051361; CG31361.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 508 AA; 54018 MW; 203110CA2A9523EE CRC64;

Query Match 55.7%; Score 58.5; DB 2; Length 508;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 16; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

OY 1 AXAEAEKAKYAAAEAKAKAX 24
Db 187 AAADAAE-AAKLAEEAAQAAAK 209

RESULT 31
O9VGD3 PRELIMINARY; PRT; 664 AA.
AC 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE CG31361-PA.
GN ORNames-CG31361;
OS Drosophila melanogaster (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abri'l J.F., Agbayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein F., Brottier P.,
RA Butts J.C., Busam D.A., Butler H., Cadieu L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos R., Delcher A., Deng X., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dushin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Foder C., Garg J., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwam C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodrager, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.U., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.U., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB003694; AAF54750.2; -
DR InterAct; O9VGD3; -
DR FlyBase; FBgn0051361; CG31361.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 664 AA; 70618 MW; 75C8A45055C457B CRC64;

Query Match 55.7%; Score 58.5; DB 2; Length 664;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 16; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

OY 1 AXAEAEKAKYAAAEAKAKAX 24
Db 343 AAADAAE-AAKLAEEAAQAAAK 365

RESULT 32
O8SWT7 PRELIMINARY; PRT; 694 AA.

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AC Q88MT7;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RES6367P.
GN Name=CG14738; ORFNames=CG31361;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Strepleton M., Brooks P., Hong L., Aghayani A., Carlson J.,
RA Campe W., Chavez C., Dorsett V., Dresnek D., Fattan D., Frise B.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragae V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY095087; AAM11415.1; -.
DR HSSP; Q9UQ9; 1EOO.
DR Flybase; FBgn0051361; CG31361.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 694 AA; 75164 MW; 9C242FP03051491 CRC64;

Query Match 55.7%; Score 58.5; DB 2; Length 694;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 16; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

Oy 1 AXAEEAKAKYAAAEAKAKAX 24
Db 343 AAADAAEAAKLAARAAQAQAAAK 365

RESULT 33
O9P3E2 PRELIMINARY; PRT; 1171 AA.
AC O9P3E2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Related to transport protein USO1.
GN Name=B13118.10;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hobeisel J., Brandt P., Fartmann B., Holland R.,
RA Nykatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390189; CAB99171.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR006955; USO1_p115_C.
DR InterPro; IPR006953; USO1_p115_head.
DR Pfam; PF04871; USO1_p115_C_1.
DR Pfam; PF04869; USO1_p115_head_1.
SQ SEQUENCE 1171 AA; 131632 MW; 33DF505E931ED060 CRC64;
```

```
Query Match 55.7%; Score 58.5; DB 2; Length 1171;
Best Local Similarity 56.7%; Pred. No. 1.2e+02;
Matches 17; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

Oy 1 AXAEEA-----AEKAKYAAAEAKAKAXA 25
Db 1025 AEAADATATGAEEKAAAEAEAAAKAAAS 1054

RESULT 34
O9DF23 PRELIMINARY; PRT; 92 AA.
ID O9DF23;
AC O9DF23;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Skin-type antifreeze polypeptide AFP-2.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottidae; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=98389738; PubMed=9722537; DOI=10.1074/jbc.273.36.23098;
RA Low W.-K., Mao M., Ewart K.V., Yang D.S.C., Fletcher G.L., Hew C.L.;
RT "Skin-type antifreeze protein from the shorthorn sculpin.
RT Myoxocephalus scorpius. Expression and characterization of a Mr 9, 700
RT recombinant protein";
RL J. Biol. Chem. 273:23098-23103 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Low W.-K., Mao M., Ewart K.V., Yang D.S.C., Fletcher G.L., Hew C.L.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305502; AAG25982.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0005825; F:ice binding; IEA.
DR GO; GO:0042309; P:homeothermy; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:00050826; P:response to freezing; IEA.
DR InterPro; IPR001044; Antifreeze_1.
DR InterPro; IPR001778; POA allergen_C.
DR InterPro; IPR001859; Ribosomal_P2.
DR PRINTS; PR00308; ANTIFREEZE1.
DR PRINTS; PR00833; POAALLERGEN.
DR PRINTS; PR00456; RIBOSOMALP2.
SQ SEQUENCE 92 AA; 7693 MW; A3FCFD57B5CA8465 CRC64;

Query Match 55.2%; Score 58; DB 2; Length 92;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Oy 1 AXAEEAKAKYAAAEAKAKAXA 25
Db 3 AAACAEEAAMAAAMAAAEAAATKAA 27

RESULT 35
O7V6K8 PRELIMINARY; PRT; 124 AA.
ID O7V6K8;
AC O7V6K8;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Type 1 antifreeze protein.
CN OrderedLocustNames=PMT1149;
OS Prochlorococcus marinus (strain MIT 9313).
```


DR PROSITE; PS50862; AA TRNA LIGASE_II; 1.
 KW Hypothetical protein; Ligase.
 SQ SEQUENCE 558 AA; 63124 MW; 9555E653E44E1A8 CRC64;
 Query Match 55.2%; Score 58; DB 2; Length 558;
 Best Local Similarity 59.1%; Pred. No. 75;
 Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 AXAAEAKAKYAAEAAEAKAK 22
 Db 10 SALKKAERAAQMAAKKAERAAK 31

RESULT 38
 Q6PF71 PRELIMINARY; PRT; 575 AA.
 AC Q6PF71;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Dichtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stadelson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Uddin T.B., Toshiyuki S., Carinci P., Prange C.,
 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Wozney K.C., Hale S., Garcia A.M., Gay L.J., Hultay S.W.,
 Villalón J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalski U., Smallus D.E., Scherch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative".
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057706; AAH57706.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003097; Pept_Aspartic.
 DR InterPro; IPR003099; Treg_SCAN.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF02023; SCAN; 1.

DR Pfam; PF00098; zf-CCHC; 1.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PROSITE; PS50804; SCAN BOX; 1.
 DR PROSITE; PS50156; ZF_CCHC; 1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 575 AA; 62786 MW; D60DF4183B8C81B6 CRC64;
 Query Match 55.2%; Score 58; DB 2; Length 575;
 Best Local Similarity 57.7%; Pred. No. 77;
 Matches 15; Conservative 6; Mismatches 3; Indels 2; Gaps 1;

QY 2 XAAEAKAKYAA--EAAEAKAKAXA 25
 Db 49 QAEEAERAAERTAEAAEAAERAAERTA 74

RESULT 39
 Q88YV9 PRELIMINARY; PRT; 660 AA.
 AC Q88YV9;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ABC transporter, ATP-binding protein.
 DE OrderedLocustNames=lp_0723;
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillius.
 NCBI_TaxID=1590;
 RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 Hoffer S.M., Nierop Groet M.N., Kerkhoven R., De Vries M., Ursing B.,
 De Vos W.M., Slezacek R.;
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1".
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
 CC -1 SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AL955253; CAD63322.1; -;
 DR HSBP; P58301; IUS8.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SMO0382; AAA; 2.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 660 AA; 74176 MW; 10783CC765A085D1 CRC64;
 Query Match 55.2%; Score 58; DB 2; Length 660;
 Best Local Similarity 63.6%; Pred. No. 86;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 EAAEAKAKYAAEAAEAKAKAXA 25
 Db 538 EQAEIAPAAAAGQAEEAKAEAGA 559

RESULT 40
 P90534 PRELIMINARY; PRT; 809 AA.
 AC P90534;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

Transmembrane.
FT CHAIN 1 423 X1 protein.
FT CHAIN 424 620 X2 protein.
FT CHAIN 621 1212 NTP-binding protein.
FT CHAIN 1213 1239 Viral genome-linked protein.
FT CHAIN 1240 1486 3C-like protease.
FT CHAIN 1487 2197 RNA-directed RNA polymerase.
FT DOMAIN 621 1167 Cytoplasmic.
FT TRANSMEM 1168 1188 Probable.
FT DOMAIN 1189 1212 Lumenal.
FT NP_BIND 796 803 ATP (potential).
FT DOMAIN 149 152 Poly-Pro.
FT DOMAIN 230 235 Poly-Pro.
FT ACT_SITE 1283 1283 3C-like protease (Probable).
FT ACT_SITE 1331 1331 3C-like protease (Potential).
FT ACT_SITE 1433 1433 3C-like protease (Potential).
FT SITE 1451 1451 Involved in the cleavage site specificity.
FT CARBOHYD 1228 1228 N-linked (GlcNAc...).
FT MUTAGEN 423 423 Missing: No cleavage between X1 and X2.
FT MUTAGEN 620 620 Missing: No cleavage between X2 and NTB.
FT MUTAGEN 1212 1212 Missing: No cleavage NTB and Vfg.
FT MUTAGEN 1230 1230 T->A: Complete loss of N-linked glycosylation.
FT MUTAGEN 1283 1283 H->D: Complete loss of protease activity.
FT MUTAGEN 1451 1451 H->L: Complete loss of protease activity.
FT MUTAGEN 1465 1465 Q->A: No effect.
FT MUTAGEN 1486 1486 Q->A: No cleavage between 3C-like protease and RNA-directed RNA polymerase.
FT CONFLICT 1230 1230 T -> A (in Ref. 4; AA sequence).
SQ SEQUENCE 2197 AA; 244128 MW; 2D8EF928E5DB089 CRC64;

Query Match 55.2%; Score 58; DB 1; Length 2197;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 6 AEKAKYAAAEAKAKAXA 25
Db 180 ARKAKYAAFAAKKAAYV 199

RESULT 42
089IE3 PRELIMINARY; PRT; 638 AA.
AC 089IE3;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE B115696 protein.
GN OrderedLocusNames=b115696;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
CX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=2248498; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiuni T.,
RA Sasaoka S., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Kohara M., Matsunoto M.,
RA Tabata S.,
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL: AP005955; BACS0961.1; -;
DR GO: GO:0030693; F:casease activity; IEA.
DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001309; ICD p20.
DR PROSITE: PS50208; CASPAGE_p20; 1.
KW Complete proteome.
SQ SEQUENCE 638 AA; 68387 MW; 9519C8A749528B5B CRC64;

Query Match 54.8%; Score 57.5; DB 2; Length 638;
Best Local Similarity 53.3%; Pred. No. 95;
Matches 16; Conservative 4; Mismatches 5; Indels 5; Gaps 1;

OY 1 AAEAAEK-----AAKYAAAEAKAKAXA 25
Db 415 AEKQAAEKAAKAEKAAKQAEKQAPAKPTA 444

RESULT 43
015860 PRELIMINARY; PRT; 190 AA.
ID 015860;
AC 015860;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Merozoite surface protein 3 (Fragment).
GN Name=SPAM;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97391128; PubMed=9247935; DOI=10.1016/S0166-6851(97)00067-4;
RA Huber W., Felger I., Matile H., Lippe H.J., Steiger S., Beck H.P.;
RT "Limited sequence polymorphism in the Plasmodium falciparum merozoite
surface protein 3.";
RL Mol. Biochem. Parasitol. 87:231-234(1997).
DR EMBL: AF001149; AAC47674.1; -;
DR InterPro: IPR010784; Merozoite SPAM.
DR Pfam: PF07133; Merozoite_SPAM; 1.
KW Merozoite.
FT NON_TER 1 1
FT NON_TER 190 190
SQ SEQUENCE 190 AA; 21170 MW; 9BD627A8758AC41C CRC64;

Query Match 54.3%; Score 57; DB 2; Length 190;
Best Local Similarity 56.5%; Pred. No. 41;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 2 XAEAAEKAKYAAAEAKAKAX 24
Db 71 AAEAAEKAAAEKAAAEKQAEKQAS 93

RESULT 44
08X965 PRELIMINARY; PRT; 394 AA.
AC 08X965;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
GN Name=cola; OrderedLocusNames=BC80774, 20907;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDJ933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Poefaj G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimatena E.T., Potamoudis K.,
RA Apodaca A., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.

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OM protein - protein search, using sw model

Run on: July 11, 2005, 09:22:59 ; Search time 161 Seconds

(without alignments)
60.056 Million cell updates/secTitle: SEQ1
Perfect score: 105
Sequence: 1 axaaakaakyaakaakaxa 25Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	25	AAB66787	AAB66787 Amphipath
2	67	63.8	104	ADK10685	Adk10685 Structura
3	67	63.8	104	ADK10635	Adk10635 Structura
4	67	63.8	104	ADK15654	Adk15654 Nucleatin
5	67	63.8	104	ADK15704	Adk15704 Library f
6	65.5	62.4	428	ABU27824	Abu27824 protein e
7	64	61.0	28	ADO43180	Ado43180 Peptide u
8	64	61.0	28	ADO43177	Ado43177 Peptide u
9	64	61.0	104	ADK10683	Adk10683 Structura
10	64	61.0	104	ADK10682	Adk10682 Structura
11	64	61.0	104	ADK10632	Adk10632 Structura
12	64	61.0	104	ADK15652	Adk15652 Nucleatin
13	64	61.0	104	ADK15701	Adk15701 Library f
14	64	61.0	104	ADK15702	Adk15702 Library f
15	64	61.0	104	ADK15651	Adk15651 Nucleatin
16	64	61.0	104	ADK15651	Adk15651 Nucleatin
17	63.5	60.5	104	ADK10684	Adk10684 Structura
18	63.5	60.5	104	ADK10634	Adk10634 Structura
19	63.5	60.5	104	ADK15703	Adk15703 Library f
20	63.5	60.5	104	ADK15653	Adk15653 Nucleatin
21	63	60.0	59	ADK10698	Adk10698 Structura
22	63	60.0	59	ADK10648	Adk10648 Structura
23	63	60.0	59	ADK15717	Adk15717 Library f
24	63	60.0	59	ADK15667	Adk15667 Nucleatin
25	63	60.0	67	ADK10697	Adk10697 Structura

26	63	60.0	67	ADK10647	Adk10647 Structura
27	63	60.0	67	ADK15666	Adk15666 Nucleatin
28	63	60.0	67	ADK15716	Adk15716 Library f
29	63	60.0	75	ADK10696	Adk10696 Structura
30	63	60.0	75	ADK10646	Adk10646 Structura
31	63	60.0	75	ADK15715	Adk15715 Library f
32	63	60.0	75	ADK15665	Adk15665 Nucleatin
33	63	60.0	83	ADK10695	Adk10695 Structura
34	63	60.0	83	ADK10645	Adk10645 Structura
35	63	60.0	83	ADK15714	Adk15714 Library f
36	63	60.0	83	ADK15664	Adk15664 Nucleatin
37	63	60.0	88	ADK10642	Adk10642 Structura
38	63	60.0	88	ADK10692	Adk10692 Structura
39	63	60.0	88	ADK15711	Adk15711 Library f
40	63	60.0	88	ADK15661	Adk15661 Nucleatin
41	63	60.0	91	ADK10694	Adk10694 Structura
42	63	60.0	91	ADK10644	Adk10644 Structura
43	63	60.0	91	ADK15663	Adk15663 Nucleatin
44	63	60.0	91	ADK15713	Adk15713 Library f
45	63	60.0	104	ADK10690	Adk10690 Structura

ALIGNMENTS

RESULT 1
AAB66787 standard; peptide; 25 AA.
XX AAB66787;
AC 11-APR-2001 (first entry)
DT 11-APR-2001 (first entry)
XX XX
DE Amphipathic peptide conjugate.
XX XX
KW Amphipathic; lipid bilayer; detergent.
XX XX
OS Synthetic.
XX XX
PN WO200102425-A2.
XX XX
PD 11-JAN-2001.
XX XX
PF 29-JUN-2000; 2000MO-CA000773.
XX XX
PR 29-JUN-1999; 99US-0140988P.
XX XX
PA (UYHE-) UNIV HEALTH NETWORK.
XX XX
PI Prive G;
XX XX
DR WPI; 2001-138120/14.
XX XX
PT New amphipathic peptide conjugate having detergent properties, and
PT hydrophobic and hydrophilic phase, useful e.g. for stabilizing and
PT crystallizing proteins and membrane proteins, as cytolytic agents,
PT surfactants or emulsifiers.
XX XX
PS Claim 1; Page 22; 29pp; English.
XX XX
CC The present invention relates to an amphipathic peptide conjugate having
CC detergent properties and a hydrophobic and hydrophilic face. The
CC amphipathic peptide conjugate may be used for the stabilization and
CC crystallization of proteins and membrane proteins, for modifying the
CC properties of lipid bilayer membranes, as cytolytic agents, as molecules
CC that can facilitate the transport of polar molecules across biological
CC membranes, and as emulsifiers and surfactants
XX XX
SQ Sequence 25 AA;
Query Match 100.0%; Score 105; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) of one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmetic applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a protein associated with
 CC fused nucleic acid and random peptide libraries of the invention.

XX SQ Sequence 104 AA;

Query Match 63.8%; Score 67; DB 7; Length 104;
 Best Local Similarity 68.0%; Pred. No. 0.18;
 Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAEAEKAKYAAEAERAKAKAXA 25
 Db 10 AAAAAEAERAKAKAEAAKAAEA 34

RESULT 4

ID ADK15654 standard; peptide; 104 AA.

XX AC ADK15654;

XX DT 06-MAY-2004 (first entry)

XX DE Nucleating sequence-containing library fusion protein #36.

XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.

XX OS Synthetic.

XX PN US2003224412-A1.

XX PD 04-DEC-2003.

XX PF 18-MAR-2003; 2003US-00393449.

XX PR 08-OCT-1998; 98US-00169015.

XX PR 08-OCT-1999; 99US-00415765.

XX PR 20-JUN-2002; 2002US-00177725.

XX PA (ANDE/) ANDERSON D.
 XX PA (PEEL/) PELLIE B R.
 XX PA (BOGE/) BOGENBERGER J M.

XX Anderson D, Peelle BR, Bogenberger JM;
 XX WPI; 2004-033956/03.

XX Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.
 XX Example 6; SEQ ID NO 42; 110pp; English.

XX The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a
 CC nucleating sequence. The library of the invention is useful for screening
 CC bioactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a library protein containing a nucleating
 CC sequence.

XX SQ Sequence 104 AA;

Query Match 63.8%; Score 67; DB 8; Length 104;
 Best Local Similarity 68.0%; Pred. No. 0.18;
 Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAEAEKAKYAAEAERAKAKAXA 25
 Db 10 AAAAAEAERAKAKAEAAKAAEA 34

RESULT 5

ID ADK15704 standard; peptide; 104 AA.

XX AC ADK15704;

XX DT 06-MAY-2004 (first entry)

XX DE Library fusion protein-related scaffold protein #36.

XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.

XX OS Synthetic.

XX PN US2003224412-A1.

XX PD 04-DEC-2003.

XX PF 18-MAR-2003; 2003US-00393449.

XX PR 08-OCT-1998; 98US-00169015.

XX PR 08-OCT-1999; 99US-00415765.

XX PR 20-JUN-2002; 2002US-00177725.

XX PA (ANDE/) ANDERSON D.
 XX PA (PEEL/) PELLIE B R.
 XX PA (BOGE/) BOGENBERGER J M.

XX Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2004-033956/03.

XX Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.
 XX Disclosure; SEQ ID NO 92; 110pp; English.

XX The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green fluorescent

CC protein - GFP) and a library peptide sequence comprising an alpha helical
CC biasing sequence, or a scaffold protein, a library peptide and a
CC nucleating sequence. The library of the invention is useful for screening
CC bioactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a scaffold protein.

XX
SQ Sequence 104 AA;

Query Match 63.8%; Score 67; DB 8; Length 104;
Best Local Similarity 68.0%; Pred. No. 0.18;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAAAEKAKYAAAEAKAKAXA 25
Db 10 AAAAAEAAKAAAEAAKAAAEAA 34

RESULT 6

ABU27824
ID ABU27824 standard; protein; 428 AA.

XX AC ABU27824;

DT 19-JUN-2003 (first entry)

DE Protein encoded by prokaryotic essential gene #13351.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Enterobacter cloacae.

XX W0200277183-A2.

XX PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.

DR N-PSDB; ACA31694.

PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 55748; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 613 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 428 AA;

Query Match 62.4%; Score 65.5; DB 6; Length 428;
Best Local Similarity 62.1%; Pred. No. 1.4;
Matches 18; Conservative 4; Mismatches 2; Indels 5; Gaps 1;

Qy 1 AXAAAEKAA-----KYAAAEKAKAX 24
Db 210 AEAABAKKAAQEAERKAAAEKAAAE 238

RESULT 7

AD043180
ID AD043180 standard; peptide; 28 AA.

XX AC AD043180;

DT 29-JUL-2004 (first entry)

DE Peptide used for coded probe synthesis.

XX Nano-barcode; scanning probe microscopy; probe.

XX Synthetic.

XX W02004038037-A2.

XX PD 06-MAY-2004.

PF 22-SEP-2003; 2003WO-US029726.

PR 20-SEP-2002; 2002US-00251152.

PR 19-SEP-2003; 2003US-00667004.

XX (ITLC) INTEL CORP.

PI Chan S, Su X, Yamakawa M;
XX WPI; 2004-399960/37.

DR WPI; 2004-399960/37.

PT Detecting, identifying and sequencing of biomolecules using controlled
PT alignment of nano-barcodes encoding specific information for scanning
PT probe microscopy, useful in the fields of molecular biology.

XX Example 2; Page 44; 63pp; English.

XX The present sequence is that of a peptide of potential use for production
CC of a coded probe useful in the method of the invention. The invention
CC provides methods, apparatus and compositions for the detection,
CC identification and/or sequencing of biomolecules, such as nucleic acids
CC or proteins. Coded probes comprising a probe molecule attached to one or
CC more nano-barcodes are allowed to bind to target molecule(s). After
CC binding and separation from unbound coded probes, the bound coded probes
CC are aligned on a surface and analysed by scanning probe microscopy (SPM).
CC The methods allow the sequencing of long nucleic acid sequences in a
CC single sequencing run, high speed of obtaining sequence data, low cost of
CC sequencing and high efficiency in terms of operator time, and sensitive

CC and accurate detection and/or identification of nucleic acids with low
CC incidence of false positive results.

XX Sequence 28 AA;

Query Match 61.0%; Score 64; DB 8; Length 28;
Best Local Similarity 65.2%; Pred. No. 0.1;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 XAEAAEKAAKYAAEAERAAKAX 24
:||||:||||:||||:||||:
Db 1 AAEAAAEAAEAEEAAEAEEAAEA 23

RESULT 8
AD043177
ID AD043177 standard; peptide; 28 AA.

AC AD043177;

DT 29-JUL-2004 (first entry)

DE Peptide used for coded probe synthesis.

KM Nano-barcode; scanning probe microscopy; probe.

OS Synthetic.

PN WO2004038037-A2.

PD 06-MAY-2004.

PF 22-SEP-2003; 2003WO-US029726.

PR 20-SEP-2002; 2002US-00251152.

PR 19-SEP-2003; 2003US-00667004.

XX (ITLC) INTEL CORP.

XX Chan S, Su X, Yamakawa M;

DR WPI; 2004-399960/37.

PT Detecting, identifying and sequencing of biomolecules using controlled
PT alignment of nano-barcodes encoding specific information for scanning
PT probe microscopy, useful in the fields of molecular biology.

PS Example 2; Page 44; 63pp; English.

XX The present sequence is that of a peptide of potential use for production
CC of a coded probe useful in the method of the invention. The invention
CC provides methods, apparatus and compositions for the detection,
CC identification and/or sequencing of biomolecules, such as nucleic acids
CC or proteins. Coded probes comprising a probe molecule attached to one or
CC more nano-barcodes are allowed to bind to target molecule(s). After
CC binding and separation from unbound coded probes, the bound coded probes
CC are aligned on a surface and analysed by scanning probe microscopy (SPM).
CC The methods allow the sequencing of long nucleic acid sequences in a
CC single sequencing run, high speed of obtaining sequence data, low cost of
CC sequencing and high efficiency in terms of operator time, and sensitive
CC and accurate detection and/or identification of nucleic acids with low
CC incidence of false positive results.

XX Sequence 28 AA;

Query Match 61.0%; Score 64; DB 8; Length 28;
Best Local Similarity 65.2%; Pred. No. 0.1;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 XAEAAEKAAKYAAEAERAAKAX 24
:||||:||||:||||:||||:
Db 1 AAEAAAEAAEAEEAAEAEEAAEA 23

RESULT 9
ADE10683
ID ADE10683 standard; protein; 104 AA.

AC ADE10683;

DT 29-JAN-2004 (first entry)

DE Structurally biased random peptide library scaffold protein seqid 90.

XX fusion nucleic acid library; scaffold protein; bioactive peptide;
KM phenotype change; cell morphology; cell growth; cell viability;
KM cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KM loss of cell division; decreased cell growth; brca-1; brca-2;
KM tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KM Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
KM skin biology; cosmetic; endocrinology; infectious disease;
KM drug toxicity; drug resistance; inflammation; allergic response;
KM scaffold protein.

OS Synthetic.

PN US2003143562-A1.

PD 31-JUL-2003.

PF 20-JUN-2002; 2002US-00177725.

PR 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

XX (RIG-) RIGEL PHARM INC.

XX Anderson D, Peelle BR, Bogenberger JM;

DR WPI; 2003-829786/77.

PT Novel library of fusion nucleic acids each of which has fused first and
PT second nucleic acids encoding scaffold protein and library peptide having
PT alpha helical biasing sequence, respectively, useful in screening
PT methods.

PS Disclosure; SEQ ID NO 90; 110pp; English.

XX The invention describes a library (1) of fusion nucleic acids, where each
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence,
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
CC peptides conferring a change in specific phenotype such as cell
CC morphology, cell growth, cell viability, adhesion to substrates or other
CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
CC lipid, hormones, cytokines, or other molecules; etc. The bioactive
CC peptide identified by above mentioned method is used to generate more
CC candidate peptides and to identify target molecules, i.e., the molecules
CC with which the bioactive peptide interacts. The peptide(s) can be
CC combined with other pharmacologic activators to study the epistatic
CC relationships of signal transduction pathways in question. The disclosed
CC method is also useful in cancer applications. Random libraries can be
CC introduced into any tumour cell (primary or cultured), and peptides
CC identified which by themselves induce apoptosis, cell death, loss of cell
CC division or decreased cell growth. The method is also useful for
CC screening of bioactive peptides which restore the constitutive function
CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
CC important in breast cancer such as the adenomatous polyposis coli gene
CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
CC cell-cell junctions. The methods are useful in cardiovascular
CC applications, neurobiology applications, bone biology applications, skin
CC biology applications, cosmetic applications, endocrinology
CC applications, infectious disease applications, drug toxicities and drug

	CC	resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a scaffold protein used in peptide libraries or hold the library peptide in a conformationally restricted form.
SQ	XX	Sequence 104 AA;
	XX	Query Match: 61.0%; Score 64; DB 7; Length 104;
	XX	Best Local Similarity 72.0%; Pred. No. 0.45;
	XX	Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1
OY		1 AXAEAAEKAKYAAEAEEAKAKAXA 25 : : 9 AAEAAKKA--AAAAEAAKAA 31
Db		
RESULT 10		
ID	ADEI0682	
XX	ADEI0682 standard; protein; 104 AA.	
AC	ADEI0682;	
XX		
DT	29-JAN-2004 (first entry)	
XX		
DE	Structurally biased random peptide library scaffold protein seqid 89.	
XX		
KM	fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability;	
KM	cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;	
KM	loss of cell division; decreased cell growth; brca-1; brca-2;	
KM	tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;	
KM	Drosophila discs-large; Dig; cardiovascular; neurobiology; bone biology;	
KM	skin biology; cosmeceutical; endocrinology; infectious disease;	
KM	drug toxicity; drug resistance; inflammation; allergic response;	
KM	scaffold protein.	
XX		
OS	Synthetic.	
XX		
FN	US2003143562-A1.	
XX		
PD	31-JUL-2003.	
XX		
PF	20-JUN-2002; 2002US-00177725.	
XX		
PR	08-OCT-1998; 98US-00169015.	
PR	08-OCT-1999; 99US-00415765.	
XX		
PA	(RIGE-) RIGEL PHARM INC.	
PI		
PI	Anderson D, Peelle BR, Bogenberger JM;	
XX		
DR	WPI; 2003-829786/77.	
XX		
PT	Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening methods.	
PT		
PS	Disclosure; SEQ ID NO 89; 110pp; English.	
XX		
CC	The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more	

CC	RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
CC	in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
CC	lipids, hormones, cytokines, or other molecules; etc. The bioactive
CC	peptide identified by above mentioned method is used to generate more
CC	candidate peptides and to identify target molecules, i.e., the molecules
CC	with which the bioactive peptide interacts. The peptide(s) can be
CC	combined with other pharmacologic activators to study the epistatic
CC	relationships of signal transduction pathways in question. The disclosed
CC	method is also useful in cancer applications. Random libraries can be
CC	introduced into any tumour cell (primary or cultured), and peptides
CC	identified which by themselves induce apoptosis, cell death, loss of cell
CC	division or decreased cell growth. The method is also useful for
CC	screening of bioactive peptides which restore the constitutive function
CC	of the bcr-1 or bcr-2 genes, and other tumour suppressor genes
CC	important in breast cancer such as the adenomatous polyposis coli gene
CC	(APC) and the Drosophila discs-large gene (Dlg), which are components of
CC	cell-cell junctions. The methods are useful in cardiovascular
CC	applications, neurobiology applications, bone biology applications, skin
CC	biology applications, cosmeceutical applications, drug toxicities and drug
CC	resistance applications, immunobiology, inflammation, and allergic
CC	response applications, and biotechnology applications. The peptide
CC	library can easily be monitored, both for its presence within cells and
CC	its quantity. The expression of structurally biased libraries generate
CC	elevated cellular concentration of peptides having a given structural
CC	bias and thus increase the hit rate for targets that bind such
CC	structures. This is the amino acid sequence of a scaffold protein used in
CC	peptide libraries or hold the library peptide in a conformationally
CC	restricted form.
CC	
SQ	Sequence 104 AA;
Query Match	61.0%; Score 64; DB 7; Length 104;
Best Local Similarity	72.0%; Pred. No. 0.45;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;	
OY	1 AXAERAERAKYAAAEAKAKAA 25
	: :
Db	9 AAAERAAKAA--AAAAEAAAKAAA 31
RESULT 11	
AD10633	
ID	AD10633 standard; protein; 104 AA.
AC	
XX	AD10633;
DT	29-JAN-2004 (first entry)
XX	
DE	Structurally biased random peptide library related protein seqid 40.
XX	
KM	fusion nucleic acid library; scaffold protein; bioactive peptide;
KM	phenotype change; cell morphology; cell growth; cell viability;
KM	cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KM	loss of cell division; decreased cell growth; bcr-1; bcr-2;
KM	tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KM	Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
KM	skin biology; cosmeceutical; endocrinology; infectious disease;
KM	drug toxicity; drug resistance; inflammation; allergic response.
XX	
OS	Synthetic.
XX	
PN	US2003143562-A1.
XX	
PD	31-JUL-2003.
XX	
PF	20-JUN-2002; 2002US-00177725.
XX	
PR	08-OCT-1998; 98US-00169015.
XX	
PR	08-OCT-1999; 99US-00415765.
XX	
PA	(RIGE-) RIGEL PHARM INC.
XX	

PI Anderson D, Peelle BR, Bogenberger JM;
 XX WPI; 2003-829786/77.
 XX
 PT Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX
 PS Example 6; SEQ ID NO 40; 110pp; English.
 XX
 CC The invention describes a library (1) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;
 CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipid, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the bcr-a-1 or bcr-a-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmetic applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a protein associated with
 CC fused nucleic acid and random peptide libraries of the invention.
 XX
 SQ Sequence 104 AA;
 Query Match 61.0%; Score 64; DB 7; Length 104;
 Best Local Similarity 72.0%; Pred. No. 0.45;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 AXAEAAEKAKYAAAEAKAKAXA 25.
 Db 9 AAAAEAAAKYA--AAAAAEAAAKAXA 31
 RESULT 12
 ADE10632 ID ADE10632 standard; protein: 104 AA.
 XX ADE10632;
 AC 29-JAN-2004 (first entry)
 DT 29-JAN-2004 (first entry)
 XX Structurally biased random peptide library related protein seqid 39.
 DE Structurally biased random peptide library related protein seqid 39.
 XX fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotypic change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; bcr-a-1; bcr-a-2;

KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmetic; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response.
 XX
 OS Synthetic.
 XX
 PN US2003143562-A1.
 XX
 PD 31-JUL-2003.
 XX
 XX 20-JUN-2002; 2002US-00177725.
 PF 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 XX
 PA (RIG-) RIGEL PHARM INC.
 PI Anderson D, Peelle BR, Bogenberger JM;
 XX WPI; 2003-829786/77.
 XX
 DR Novel library of fusion nucleic acids each of which has fused first and
 XX second nucleic acids encoding scaffold protein and library peptide having
 XX alpha helical biasing sequence, respectively, useful in screening
 XX methods.
 PT
 PT Example 6; SEQ ID NO 39; 110pp; English.
 XX
 PS The invention describes a library (1) of fusion nucleic acids, where each
 PS fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 PS scaffold protein sequence; and a second nucleic acid (N2), encoding a
 PS library peptide sequence comprising an alpha helical biasing sequence;
 PS where N1 is fused to N2. Disclosed is a method for screening bioactive
 PS peptides conferring a change in specific phenotype such as cell
 PS morphology, cell growth, cell viability, adhesion to substrates or other
 PS cells, and cellular density; changes in the expression of one or more
 PS RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 PS in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 PS lipid, hormones, cytokines, or other molecules; etc. The bioactive
 PS peptide identified by above mentioned method is used to generate more
 PS candidate peptides and to identify target molecules, i.e., the molecules
 PS with which the bioactive peptide interacts. The peptide(s) can be
 PS combined with other pharmacologic activators to study the epistatic
 PS relationships of signal transduction pathways in question. The disclosed
 PS method is also useful in cancer applications. Random libraries can be
 PS introduced into any tumour cell (primary or cultured), and peptides
 PS identified which by themselves induce apoptosis, cell death, loss of cell
 PS division or decreased cell growth. The method is also useful for
 PS screening of bioactive peptides which restore the constitutive function
 PS of the bcr-a-1 or bcr-a-2 genes, and other tumour suppressor genes
 PS important in breast cancer such as the adenomatous polyposis coli gene
 PS (APC) and the Drosophila discs-large gene (Dlg), which are components of
 PS cell-cell junctions. The methods are useful in cardiovascular
 PS applications, neurobiology applications, bone biology applications, skin
 PS biology applications, cosmetic applications, endocrinology
 PS applications, infectious disease applications, drug toxicities and drug
 PS resistance applications, immunobiology, inflammation, and allergic
 PS response applications, and biotechnology applications. The peptide
 PS library can easily be monitored, both for its presence within cells and
 PS its quantity. The expression of structurally biased libraries generate
 PS elevated cellular concentration of peptides having a given structural
 PS bias and thus increase the hit rate for targets that bind such
 PS structures. This is the amino acid sequence of a protein associated with
 PS fused nucleic acid and random peptide libraries of the invention.
 XX
 SQ Sequence 104 AA;
 Query Match 61.0%; Score 64; DB 7; Length 104;
 Best Local Similarity 72.0%; Pred. No. 0.45;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 AXAEAAEKAKYAAAEAKAKAXA 25

Db 9 AAAAAAAAAA-AAAAAAAAA 31

RESULT 13

ADK15652

ID ADK15652 standard; peptide; 104 AA.

AC ADK15652;

DT 06-MAY-2004 (first entry)

DB Nucleating sequence-containing library fusion protein #34.

XX fusion nucleic acid library; fusion protein library; scaffold protein;

KM green fluorescent protein; GFP; alpha helical biasing sequence;

XX nucleating sequence; screening.

OS Synthetic.

PN US2003224412-A1.

PD 04-DEC-2003.

PF 18-MAR-2003; 2003US-00393449.

PR 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

PR 20-JUN-2002; 2002US-00177725.

XX (ANDE/) ANDERSON D.

PA (PEEL/) PELLIE B R.

PA (BOGE/) BOGENBERGER J M.

PI Anderson D, Peelle BR, Bogenberger JM;

PS WPI; 2004-033956/03.

XX Library of fusion polypeptides in which each polypeptide comprises

PT scaffold protein and library peptide having alpha helical biasing

XX sequence, or scaffold protein, library peptide and nucleating sequence.

XX Example 6; SEQ ID NO 40; 110bp; English.

XX The invention comprises a library of fusion nucleic acids, where each

CC encoded protein contains a scaffold protein (e.g. a green fluorescent

CC protein - GFP) and a library peptide sequence comprising an alpha helical

CC biasing sequence, or a scaffold protein, a library peptide and a

CC nucleating sequence. The library of the invention is useful for screening

CC bioactive peptides conferring a particular phenotype. The present amino

CC acid sequence represents a library protein containing a nucleating

CC sequence.

XX Sequence 104 AA;

SQ Query Match 61.0%; Score 64; DB 8; Length 104;

DB Best Local Similarity 72.0%; Pred. No. 0.45;

Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Oy 1 AAAAAAAAAA-AAAAAAAAA 25

Db 9 AAAAAAAAAA-AAAAAAAAA 31

RESULT 14

ADK15701

ID ADK15701 standard; peptide; 104 AA.

XX ADK15701;

XX 06-MAY-2004 (first entry)

XX Library fusion protein-related scaffold protein #33.

XX fusion nucleic acid library; fusion protein library; scaffold protein;

KM green fluorescent protein; GFP; alpha helical biasing sequence;

XX nucleating sequence; screening.

OS Synthetic.

PN US2003224412-A1.

PD 04-DEC-2003.

PF 18-MAR-2003; 2003US-00393449.

PR 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

PR 20-JUN-2002; 2002US-00177725.

XX (ANDE/) ANDERSON D.

PA (PEEL/) PELLIE B R.

PA (BOGE/) BOGENBERGER J M.

PI Anderson D, Peelle BR, Bogenberger JM;

PS WPI; 2004-033956/03.

XX Library of fusion polypeptides in which each polypeptide comprises

PT scaffold protein and library peptide having alpha helical biasing

XX sequence, or scaffold protein, library peptide and nucleating sequence.

XX Disclosure; SEQ ID NO 89; 110bp; English.

XX The invention comprises a library of fusion nucleic acids, where each

CC encoded protein contains a scaffold protein (e.g. a green fluorescent

CC protein - GFP) and a library peptide sequence comprising an alpha helical

CC biasing sequence, or a scaffold protein, a library peptide and a

CC nucleating sequence. The library of the invention is useful for screening

CC bioactive peptides conferring a particular phenotype. The present amino

CC acid sequence represents a scaffold protein.

XX Sequence 104 AA;

SQ Query Match 61.0%; Score 64; DB 8; Length 104;

DB Best Local Similarity 72.0%; Pred. No. 0.45;

Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Oy 1 AAAAAAAAAA-AAAAAAAAA 25

Db 9 AAAAAAAAAA-AAAAAAAAA 31

RESULT 15

ADK15702

ID ADK15702 standard; peptide; 104 AA.

AC ADK15702;

DT 06-MAY-2004 (first entry)

DB Library fusion protein-related scaffold protein #34.

XX fusion nucleic acid library; fusion protein library; scaffold protein;

KM green fluorescent protein; GFP; alpha helical biasing sequence;

XX nucleating sequence; screening.

OS Synthetic.

PN US2003224412-A1.

PD 04-DEC-2003.

PF 18-MAR-2003; 2003US-00393449.

PR 08-OCT-1998; 98US-00169015.

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PR 08-OCT-1999; 99US-00415765.
PR 20-JUN-2002; 2002US-00177725.
XX
XX
PA (ANDE/) ANDERSON D.
PA (PEEL/) PEELE B R.
PA (BOGE/) BOGENBERGER J M.
XX
PI Anderson D, Peelle BR, Bogenberger JM;
XX
XX WPI; 2004-033956/03.
XX
XX Library of fusion polypeptides in which each polypeptide comprises
XX scaffold protein and library peptide having alpha helical biasing
XX sequence, or scaffold protein, library peptide and nucleating sequence.
XX
XX Disclosure; SEQ ID NO 90; 110pp; English.
XX
XX The invention comprises a library of fusion nucleic acids, where each
XX encoded protein contains a scaffold protein (e.g. a green fluorescent
XX protein - GFP) and a library peptide sequence comprising an alpha helical
XX biasing sequence, or a scaffold protein, a library peptide and a
XX nucleating sequence. The library of the invention is useful for screening
XX bioactive peptides conferring a particular phenotype. The present amino
XX acid sequence represents a scaffold protein.
XX
SQ Sequence 104 AA;

Query Match 61.0%; Score 64; DB 8; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.45;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 AXAEMAEKAKYAAEMAEKAKAXA 25
   ||||| ||| ||||| |||
Db 9 AAEMAEKAKA--AAEMAEKAKAA 31

RESULT 16
ID ADK15651 standard; peptide; 104 AA.
XX
XX ADK15651;
XX
XX 06-MAY-2004 (first entry)
XX
XX Nucleating sequence-containing library fusion protein #33.
XX
XX fusion nucleic acid library; fusion protein library; scaffold protein;
XX green fluorescent protein; GFP; alpha helical biasing sequence;
XX nucleating sequence; screening.
XX
XX Synthetic.
XX
XX US2003224412-A1.
XX
XX 04-DEC-2003.
XX
XX 18-MAR-2003; 2003US-00393449.
XX
XX 08-OCT-1998; 98US-00169015.
XX 08-OCT-1999; 99US-00415765.
XX 20-JUN-2002; 2002US-00177725.
XX
XX (ANDE/) ANDERSON D.
XX (PEEL/) PEELE B R.
XX (BOGE/) BOGENBERGER J M.
XX
XX Anderson D, Peelle BR, Bogenberger JM;
XX
XX WPI; 2004-033956/03.
XX
XX Library of fusion polypeptides in which each polypeptide comprises
XX scaffold protein and library peptide having alpha helical biasing
XX sequence, or scaffold protein, library peptide and nucleating sequence.
XX

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XX
XX Example 6; SEQ ID NO 39; 110pp; English.
XX
XX The invention comprises a library of fusion nucleic acids, where each
XX encoded protein contains a scaffold protein (e.g. a green fluorescent
XX protein - GFP) and a library peptide sequence comprising an alpha helical
XX biasing sequence, or a scaffold protein, a library peptide and a
XX nucleating sequence. The library of the invention is useful for screening
XX bioactive peptides conferring a particular phenotype. The present amino
XX acid sequence represents a library protein containing a nucleating
XX sequence.
XX
SQ Sequence 104 AA;

Query Match 61.0%; Score 64; DB 8; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.45;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 AXAEMAEKAKYAAEMAEKAKAXA 25
   ||||| ||| ||||| |||
Db 9 AAEMAEKAKA--AAEMAEKAKAA 31

RESULT 17
ID ADE10684 standard; protein; 104 AA.
XX
XX ADE10684;
XX
XX 29-JAN-2004 (first entry)
XX
XX Structurally biased random peptide library scaffold protein seqid 91.
XX
XX fusion nucleic acid library; scaffold protein; bioactive peptide;
XX phenotype change; cell morphology; cell growth; cell viability;
XX cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
XX loss of cell division; decreased cell growth; bcr-a-1; bcr-a-2;
XX tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
XX Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
XX skin biology; cosmetic; endocrinology; infectious disease;
XX drug toxicity; drug resistance; inflammation; allergic response;
XX scaffold protein.
XX
XX Synthetic.
XX
XX US2003143562-A1.
XX
XX 31-JUL-2003.
XX
XX 20-JUN-2002; 2002US-00177725.
XX
XX 08-OCT-1998; 98US-00169015.
XX 08-OCT-1999; 99US-00415765.
XX
XX (RIGE-) RIGEL PHARM INC.
XX
XX Anderson D, Peelle BR, Bogenberger JM;
XX
XX WPI; 2003-829786/77.
XX
XX Novel library of fusion nucleic acids each of which has fused first and
XX second nucleic acids encoding scaffold protein and library peptide having
XX alpha helical biasing sequence, respectively, useful in screening
XX methods.
XX
XX Disclosure; SEQ ID NO 91; 110pp; English.
XX
XX The invention describes a library (1) of fusion nucleic acids, where each
XX fusion nucleic acid comprises a first nucleic acid (N1), encoding a
XX scaffold protein sequence; and a second nucleic acid (N2), encoding a
XX library peptide sequence comprising an alpha helical biasing sequence;
XX where N1 is fused to N2. Disclosed is a method for screening bioactive
XX peptides conferring a change in specific phenotype such as cell
XX

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morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the bcr-a-1 or bcr-a-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coli gene (APC) and the Drosophila discs-large gene (Dlg), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin biology applications, infectious disease applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a scaffold protein used in peptide libraries or hold the library peptide in a conformationally restricted form.

Sequence 104 AA;

Query Match 60.5%; Score 63.5; DB 7; Length 104;

Best Local Similarity 72.0%; Pred. No. 0.52; Mismatches 4; Indels 1; Gaps 1;

Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 1 AXAEEAKYAAEAAEAKAXA 25
 6 AAAAAAEEAAK-AAAAAEEAAKAA 29

RESULT 18

ADK10634 standard; protein; 104 AA.

ADK10634;

29-JAN-2004 (first entry)

Structurally biased random peptide library related protein seqid 41.

fusion nucleic acid library; scaffold protein; bioactive peptide;
 phenotype change; cell morphology; cell growth; cell viability;
 cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 loss of cell division; decreased cell growth; bcr-a-1; bcr-a-2;
 tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
 skin biology; cosmetic; endocrinology; infectious disease;
 drug toxicity; drug resistance; inflammation; allergic response.

Synthetic.

US2003143562-A1.

31-JUL-2003.

20-JUN-2002; 2002US-00177725.

08-OCT-1998; 98US-00169015.
 08-OCT-1999; 99US-00415765.

(RIGE-) RIGEL PHARM INC.
 Anderson D, Peele BR, Bogenberger JW;
 WPI; 2003-829786/77.
 Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening methods.

Example 6; SEQ ID NO 41; 110pp; English.

The invention describes a library (1) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence, and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the bcr-a-1 or bcr-a-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coli gene (APC) and the Drosophila discs-large gene (Dlg), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin biology applications, infectious disease applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.

Sequence 104 AA;

Query Match 60.5%; Score 63.5; DB 7; Length 104;

Best Local Similarity 72.0%; Pred. No. 0.52; Mismatches 4; Indels 1; Gaps 1;

Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 1 AXAEEAKYAAEAAEAKAXA 25
 6 AAAAAAEEAAK-AAAAAEEAAKAA 29

RESULT 19

ADK15703 standard; peptide; 104 AA.

ADK15703;

06-MAY-2004 (first entry)

Library fusion protein-related scaffold protein #35.

fusion nucleic acid library; fusion protein library; scaffold protein;
 green fluorescent protein; GFP; alpha helical biasing sequence;

PT alpha helical biasing sequence, respectively, useful in screening
PT methods.
PS Disclosure; SEQ ID NO 105; 110pp; English.
XX
XX
XX The invention describes a library (1) of fusion nucleic acids, where each
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence;
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
CC peptides conferring a change in specific phenotype such as cell
CC morphology, cell growth, cell viability, adhesion to substrates or other
CC cells, and cellular density; changes in the expression of one or more
CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
CC peptide identified by above mentioned method is used to generate more
CC candidate peptides and to identify target molecules, i.e., the molecules
CC with which the bioactive peptide interacts. The peptide(s) can be
CC combined with other pharmacologic activators to study the epistatic
CC relationships of signal transduction pathways in question. The disclosed
CC method is also useful in cancer application. Random libraries can be
CC introduced into any tumour cell (primary or cultured), and peptides
CC identified which by themselves induce apoptosis, cell death, loss of cell
CC division or decreased cell growth. The method is also useful for
CC screening of bioactive peptides which restore the constitutive function
CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
CC important in breast cancer such as the adenomatous polyposis coli gene
CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
CC cell-cell junctions. The methods are useful in cardiovascular
CC applications, neurobiology applications, bone biology applications, skin
CC biology applications, cosmetic applications, endocrinology
CC applications, infectious disease applications, drug toxicities and drug
CC resistance applications, immunobiology, inflammation, and allergic
CC response applications, and biotechnology applications. The peptide
CC library can easily be monitored, both for its presence within cells and
CC its quantity. The expression of structurally biased libraries generate
CC elevated cellular concentration of peptides having a given structural
CC bias and thus increase the hit rate for targets that bind such
CC structures. This is the amino acid sequence of a scaffold protein used in
CC peptide libraries or hold the library peptide in a conformationally
CC restricted form.
CC
CC
XX
XX Sequence 59 AA;
SQ
Query Match 60.0%; Score 63; DB 7; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.32;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 2 XAENAEKAKYAAEAERAKAXA 25
: ||| ||| ||| ||| :
Db 4 DAAAEAAAKAAEAERAKAAEA 27
RESULT 22
ADE10648
ID ADE10648 standard; protein, 59 AA.
XX
XX ADE10648;
AC
XX 29-JAN-2004 (first entry)
DT
XX
XX Structurally biased random peptide library related protein seqid 55.
DE
XX fusion nucleic acid library; scaffold protein; bioactive peptide;
KW phenotype change; cell morphology; cell growth; cell viability;
KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KW loss of cell division; decreased cell growth; brca-1; brca-2;
KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KW Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
KW skin biology; cosmetic; endocrinology; infectious disease;
KW drug toxicity; drug resistance; inflammation; allergic response.
XX

OS Synthetic.
XX
XX US2003143562-A1.
PN
XX 31-JUL-2003.
XX
XX 20-JUN-2002; 2002US-00177725.
PF
XX 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
XX
XX (RIGG-) RIGEL PHARM INC.
XX
XX Anderson D, Peelie BR, Bogenberger JM;
PI WPI; 2003-829786/77.
DR
XX
XX Novel library of fusion nucleic acids each of which has fused first and
PT second nucleic acids encoding scaffold protein and library peptide having
PT alpha helical biasing sequence, respectively, useful in screening
PT methods.
PS Example 6; SEQ ID NO 55; 110pp; English.
XX
XX The invention describes a library (1) of fusion nucleic acids, where each
XX fusion nucleic acid comprises a first nucleic acid (N1), encoding a
XX scaffold protein sequence; and a second nucleic acid (N2), encoding a
XX library peptide sequence comprising an alpha helical biasing sequence;
XX where N1 is fused to N2. Disclosed is a method for screening bioactive
XX peptides conferring a change in specific phenotype such as cell
XX morphology, cell growth, cell viability, adhesion to substrates or other
XX cells, and cellular density; changes in the expression of one or more
XX RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
XX in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
XX lipids, hormones, cytokines, or other molecules; etc. The bioactive
XX peptide identified by above mentioned method is used to generate more
XX candidate peptides and to identify target molecules, i.e., the molecules
XX with which the bioactive peptide interacts. The peptide(s) can be
XX combined with other pharmacologic activators to study the epistatic
XX relationships of signal transduction pathways in question. The disclosed
XX method is also useful in cancer applications. Random libraries can be
XX introduced into any tumour cell (primary or cultured), and peptides
XX identified which by themselves induce apoptosis, cell death, loss of cell
XX division or decreased cell growth. The method is also useful for
XX screening of bioactive peptides which restore the constitutive function
XX of the brca-1 or brca-2 genes, and other tumour suppressor genes
XX important in breast cancer such as the adenomatous polyposis coli gene
XX (APC) and the Drosophila discs-large gene (Dlg), which are components of
XX cell-cell junctions. The methods are useful in cardiovascular
XX applications, neurobiology applications, bone biology applications, skin
XX biology applications, cosmetic applications, endocrinology
XX applications, infectious disease applications, drug toxicities and drug
XX resistance applications, immunobiology, inflammation, and allergic
XX response applications, and biotechnology applications. The peptide
XX library can easily be monitored, both for its presence within cells and
XX its quantity. The expression of structurally biased libraries generate
XX elevated cellular concentration of peptides having a given structural
XX bias and thus increase the hit rate for targets that bind such
XX structures. This is the amino acid sequence of a protein associated with
XX fused nucleic acid and random peptide libraries of the invention.
XX
XX
SQ Sequence 59 AA;
XX
XX
Query Match 60.0%; Score 63; DB 7; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.32;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 2 XAENAEKAKYAAEAERAKAXA 25
: ||| ||| ||| ||| :
Db 4 DAAAEAAAKAAEAERAKAAEA 27
RESULT 23

```

ADK15717
ID ADK15717 standard; peptide: 59 AA.
XX
AC ADK15717;
XX
DT 06-MAY-2004 (first entry)
XX
DE Library fusion protein-related scaffold protein #49.
XX
KM fusion nucleic acid library; fusion protein library; scaffold protein;
KM green fluorescent protein; GFP; alpha helical biasing sequence;
KM nucleating sequence; screening.
XX
OS Synthetic.
XX
PN US2003224412-A1.
XX
PD 04-DEC-2003.
XX
PF 18-MAR-2003; 2003US-00393449.
XX
PR 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
PR 20-JUN-2002; 2002US-00177725.
XX
PA (ANDE/) ANDERSON D.
PA (PEEL/) PELLIE B R.
PA (BOGE/) BOGENBERGER J M.
XX
PI Anderson D, Peelle BR, Bogenberger JM;
XX
DR WPI; 2004-033956/03.
XX
PT Library of fusion polypeptides in which each polypeptides comprises
PT scaffold protein and library peptide having alpha helical biasing
PT sequence, or scaffold protein, library peptide and nucleating sequence.
XX
PS Disclosure; SEQ ID NO 105; 110pp; English.
XX
CC The invention comprises a library of fusion nucleic acids, where each
CC encoded protein contains a scaffold protein (e.g. a green fluorescent
CC protein - GFP) and a library peptide sequence comprising an alpha helical
CC biasing sequence, or a scaffold protein, a library peptide and a
CC nucleating sequence. The library of the invention is useful for screening
CC bioactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a scaffold protein.
XX
SQ Sequence 59 AA;

Query Match 60.0%; Score 63; DB 8; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.32;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEEAKYAAAEAKAKAXA 25
Db 4 DAAAEAAKAAAEAAKAAAEAA 27

RESULT 24
ADK15667
ID ADK15667 standard; peptide: 59 AA.
XX
AC ADK15667;
XX
DT 06-MAY-2004 (first entry)
XX
DE Nucleating sequence-containing library fusion protein #49.
XX
KM fusion nucleic acid library; fusion protein library; scaffold protein;
KM green fluorescent protein; GFP; alpha helical biasing sequence;
KM nucleating sequence; screening.
XX
OS Synthetic.

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```

XX
PN US2003224412-A1.
XX
PD 04-DEC-2003.
XX
PF 18-MAR-2003; 2003US-00393449.
XX
PR 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
PR 20-JUN-2002; 2002US-00177725.
XX
PA (ANDE/) ANDERSON D.
PA (PEEL/) PELLIE B R.
PA (BOGE/) BOGENBERGER J M.
XX
PI Anderson D, Peelle BR, Bogenberger JM;
XX
DR WPI; 2004-033956/03.
XX
PT Library of fusion polypeptides in which each polypeptides comprises
PT scaffold protein and library peptide having alpha helical biasing
PT sequence, or scaffold protein, library peptide and nucleating sequence.
XX
PS Example 6; SEQ ID NO 55; 110pp; English.
XX
CC The invention comprises a library of fusion nucleic acids, where each
CC encoded protein contains a scaffold protein (e.g. a green fluorescent
CC protein - GFP) and a library peptide sequence comprising an alpha helical
CC biasing sequence, or a scaffold protein, a library peptide and a
CC nucleating sequence. The library of the invention is useful for screening
CC bioactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a library protein containing a nucleating
CC sequence.
XX
SQ Sequence 59 AA;

Query Match 60.0%; Score 63; DB 8; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.32;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEEAKYAAAEAKAKAXA 25
Db 4 DAAAEAAKAAAEAAKAAAEAA 27

RESULT 25
ADE10697
ID ADE10697 standard; protein: 67 AA.
XX
AC ADE10697;
XX
DT 29-JAN-2004 (first entry)
XX
DE Structurally biased random peptide library scaffold protein seqid 104.
XX
KM fusion nucleic acid library; scaffold protein; bioactive peptide;
KM phenotype change; cell morphology; cell growth; cell viability;
KM cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KM loss of cell division; decreased cell growth; brca-1; brca-2;
KM tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KM Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
KM skin biology; cosmetic; endocrinology; infectious disease;
KM drug toxicity; drug resistance; inflammation; allergic response;
KM scaffold protein.
XX
OS Synthetic.
XX
PN US2003143562-A1.
XX
PD 31-JUL-2003.
XX
PF 20-JUN-2002; 2002US-00177725.

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Query Match 60.0%; Score 63; DB 7; Length 67;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEEAKAKYAAEAKAKAXA 25
: ||| ||| ||| ||| :
4 DAAAEAAAKAAEAAKAAAEAA 27

Db

RESULT 27
ADK15666
ID ADK15666 standard; peptide; 67 AA.
XX
AC ADK15666;
XX
DT 06-MAY-2004 (first entry)
XX
DE Nucleating sequence-containing library fusion protein #48.
XX
KM fusion nucleic acid library; fusion protein library; scaffold protein;
KM green fluorescent protein; GFP; alpha helical biasing sequence;
KM nucleating sequence; screening.
XX
OS Synthetic.
XX
PA US2003224412-A1.
XX
PN 04-DEC-2003.
XX
PD 18-MAR-2003; 2003US-00393449.
XX
PF 08-OCT-1998; 98US-00169015.
XX
PR 08-OCT-1999; 99US-00415765.
XX
PT 20-JUN-2002; 2002US-00177725.
XX
PA (ANDE/) ANDERSON D.
PA (PEEL/) PEELE B R.
PA (BOGE/) BOGENBERGER J M.
XX
PI Anderson D, Peelle BR, Bogenberger JM;
XX
DR WPI; 2004-033956/03.
XX
XX Library of fusion polypeptides in which each polypeptides comprises
PT scaffold protein and library peptide having alpha helical biasing
PT sequence, or scaffold protein, library peptide and nucleating sequence.
XX
PS Example 6; SEQ ID NO 54; 110pp; English.
XX
XX The invention comprises a library of fusion nucleic acids, where each
CC encoded protein contains a scaffold protein (e.g. a green fluorescent
CC protein - GFP) and a library peptide sequence comprising an alpha helical
CC biasing sequence, or a scaffold protein, a library peptide and a
CC nucleating sequence. The library of the invention is useful for screening
CC bioactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a library protein containing a nucleating
CC sequence.
XX
SQ Sequence 67 AA;

Query Match 60.0%; Score 63; DB 8; Length 67;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEEAKAKYAAEAKAKAXA 25
: ||| ||| ||| ||| :
4 DAAAEAAAKAAEAAKAAAEAA 27

Db

RESULT 28
ADK15716
ID ADK15716 standard; peptide; 67 AA.

XX
AC ADK15716;
XX
DT 06-MAY-2004 (first entry)
XX
DE Library fusion protein-related scaffold protein #48.
XX
KM fusion nucleic acid library; fusion protein library; scaffold protein;
KM green fluorescent protein; GFP; alpha helical biasing sequence;
KM nucleating sequence; screening.
XX
OS Synthetic.
XX
PA US2003224412-A1.
XX
PN 04-DEC-2003.
XX
PD 18-MAR-2003; 2003US-00393449.
XX
PF 08-OCT-1998; 98US-00169015.
XX
PR 08-OCT-1999; 99US-00415765.
XX
PT 20-JUN-2002; 2002US-00177725.
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PA (ANDE/) ANDERSON D.
PA (PEEL/) PEELE B R.
PA (BOGE/) BOGENBERGER J M.
XX
PI Anderson D, Peelle BR, Bogenberger JM;
XX
DR WPI; 2004-033956/03.
XX
XX Library of fusion polypeptides in which each polypeptides comprises
PT scaffold protein and library peptide having alpha helical biasing
PT sequence, or scaffold protein, library peptide and nucleating sequence.
XX
PS Disclosure; SEQ ID NO 104; 110pp; English.
XX
XX The invention comprises a library of fusion nucleic acids, where each
CC encoded protein contains a scaffold protein (e.g. a green fluorescent
CC protein - GFP) and a library peptide sequence comprising an alpha helical
CC biasing sequence, or a scaffold protein, a library peptide and a
CC nucleating sequence. The library of the invention is useful for screening
CC bioactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a scaffold protein.
XX
SQ Sequence 67 AA;

Query Match 60.0%; Score 63; DB 8; Length 67;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEEAKAKYAAEAKAKAXA 25
: ||| ||| ||| ||| :
4 DAAAEAAAKAAEAAKAAAEAA 27

Db

RESULT 29
ADE10696
ID ADE10696 standard; protein; 75 AA.
XX
AC ADE10696;
XX
DT 29-JAN-2004 (first entry)
XX
DE Structurally biased random peptide library scaffold protein seqid 103.
XX
KM fusion nucleic acid library; scaffold protein; bioactive peptide;
KM phenotype change; cell morphology; cell growth; cell viability;
KM cell adhesion; cellular density; cancer; tumor; apoptosis; cell death;
KM loss of cell division; decreased cell growth; brca-1; brca-2;
KM tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KM Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
KM skin biology; cosmetic; endocrinology; infectious disease;

KW drug toxicity; drug resistance; inflammation; allergic response;
KM scaffold protein.
XX
OS Synthetic.
XX
PN US2003143562-A1.
XX
PD 31-JUL-2003.
XX
PF 20-JUN-2002; 2002US-00177725.
XX
PR 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
XX
PA (RIGE-) RIGEL PHARM INC.
PI Anderson D, Peelie BR, Bogenberger JM;
XX WPI; 2003-829786/77.
XX
DR Novel library of fusion nucleic acids each of which has fused first and
PT second nucleic acids encoding scaffold protein and library peptide having
PT alpha helical biasing sequence, respectively, useful in screening
PT methods.
XX
PS Disclosure; SEQ ID NO 103; 110pp; English.
XX
XX The invention describes a library (I) of fusion nucleic acids, where each
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence;
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
CC peptides conferring a change in specific phenotype such as cell
CC morphology, cell growth, cell viability, adhesion to substrates or other
CC cells, and cellular density; changes in the expression of one or more
CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
CC peptide identified by above mentioned method is used to generate more
CC candidate peptides and to identify target molecules, i.e., the molecules
CC with which the bioactive peptide interacts. The peptide(s) can be
CC combined with other pharmacologic activators to study the epistatic
CC relationships of signal transduction pathways in question. The disclosed
CC method is also useful in cancer applications. Random libraries can be
CC introduced into any tumour cell (primary or cultured), and peptides
CC identified which by themselves induce apoptosis, cell death, loss of cell
CC division or decreased cell growth. The method is also useful for
CC screening of bioactive peptides which restore the constitutive function
CC of the bcr-a-1 or bcr-a-2 genes, and other tumour suppressor genes
CC important in breast cancer such as the adenomatous polyposis coli gene
CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
CC cell-cell junctions. The methods are useful in cardiovascular
CC applications, neurobiology applications, bone biology applications, skin
CC biology applications, cosmetical applications, endocrinology
CC applications, infectious disease applications, drug toxicities and drug
CC resistance applications, immunobiology, inflammation, and allergic
CC response applications, and biotechnology applications. The peptide
CC library can easily be monitored, both for its presence within cells and
CC its quantity. The expression of structurally biased libraries generate
CC elevated cellular concentration of peptides having a given structural
CC bias and thus increase the hit rate for targets that bind such
CC structures. This is the amino acid sequence of a scaffold protein used in
CC peptide libraries or hold the library peptide in a conformationally
CC restricted form.
XX
SQ Sequence 75 AA;
XX
Query Match 60.0%; Score 63; DB 7; Length 75;
Best Local Similarity 66.7%; Pred. No. 0.42;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX
2 XAEMAEKAAKAAAEKAAKAA 25
:| ||| ||| ||| ||| ||| :|

DB 4 DAAAEAAKAAAEKAAAEKAA 27
RESULT 30
ADE10646
ID ADE10646 standard; protein; 75 AA.
XX
XX ADE10646;
XX
XX 29-JAN-2004 (first entry)
XX
DE Structurally biased random peptide library related protein seqd 53.
XX
XX fusion nucleic acid library; scaffold protein; bioactive peptide;
KW phenotype change; cell morphology; cell growth; cell viability;
KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KW loss of cell division; decreased cell growth; bcr-a-1; bcr-a-2;
KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KW Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
KW skin biology; cosmetical; endocrinology; infectious disease;
KW drug toxicity; drug resistance; inflammation; allergic response.
XX
OS Synthetic.
XX
XX US2003143562-A1.
XX
XX 31-JUL-2003.
XX
XX 20-JUN-2002; 2002US-00177725.
XX
XX 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
XX
XX (RIGE-) RIGEL PHARM INC.
PA
PI Anderson D, Peelie BR, Bogenberger JM;
XX WPI; 2003-829786/77.
XX
XX Novel library of fusion nucleic acids each of which has fused first and
PT second nucleic acids encoding scaffold protein and library peptide having
PT alpha helical biasing sequence, respectively, useful in screening
PT methods.
XX
XX Example 6; SEQ ID NO 53; 110pp; English.
XX
XX The invention describes a library (I) of fusion nucleic acids, where each
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence;
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
CC peptides conferring a change in specific phenotype such as cell
CC morphology, cell growth, cell viability, adhesion to substrates or other
CC cells, and cellular density; changes in the expression of one or more
CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
CC peptide identified by above mentioned method is used to generate more
CC candidate peptides and to identify target molecules, i.e., the molecules
CC with which the bioactive peptide interacts. The peptide(s) can be
CC combined with other pharmacologic activators to study the epistatic
CC relationships of signal transduction pathways in question. The disclosed
CC method is also useful in cancer applications. Random libraries can be
CC introduced into any tumour cell (primary or cultured), and peptides
CC identified which by themselves induce apoptosis, cell death, loss of cell
CC division or decreased cell growth. The method is also useful for
CC screening of bioactive peptides which restore the constitutive function
CC of the bcr-a-1 or bcr-a-2 genes, and other tumour suppressor genes
CC important in breast cancer such as the adenomatous polyposis coli gene
CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
CC cell-cell junctions. The methods are useful in cardiovascular
CC applications, neurobiology applications, bone biology applications, skin
CC biology applications, cosmetical applications, endocrinology

CC applications, infectious disease applications, drug toxicities and drug
CC resistance applications, immunobiology, inflammation, and allergic
CC response applications, and biotechnology applications. The peptide
CC library can easily be monitored, both for its presence within cells and
CC its quantity. The expression of structurally biased libraries generate
CC elevated cellular concentration of peptides having a given structural
CC bias and thus increase the hit rate for targets that bind such
CC structures. This is the amino acid sequence of a protein associated with
CC fused nucleic acid and random peptide libraries of the invention.

XX Sequence 75 AA;

Query Match 60.0%; Score 63; DB 7; Length 75;

Best Local Similarity 66.7%; Pred. No. 0.42; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEAEKAKYAAAEAKAKAXA 25
: ||| ||| ||| ||| :
Db 4 DAAAEAAAKAAAEAAKAAAEAA 27

RESULT 31

ADK15715 ID ADK15715 standard; peptide; 75 AA.

AC ADK15715;

DT 06-MAY-2004 (first entry)

XX Library fusion protein-related scaffold protein #47.

XX fusion nucleic acid library; fusion protein library; scaffold protein;
KW green fluorescent protein; GFP; alpha helical biasing sequence;
XX nucleating sequence; screening.

OS Synthetic.

XX US2003224412-A1.

XX 04-DEC-2003.

PF 18-MAR-2003; 2003US-00393449.

PR 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

PR 20-JUN-2002; 2002US-00177725.

XX (ANDE/) ANDERSON D.

PA (PEEL/) PEELE B R.

PA (BOGE/) BOGENBERGER J M.

PI Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2004-033956/03.

XX Library of fusion polypeptides in which each polypeptides comprises

PT scaffold protein and library peptide having alpha helical biasing

PT sequence, or scaffold protein, library peptide and nucleating sequence.

XX Disclosure; SEQ ID NO 103; 110pp; English.

XX The invention comprises a library of fusion nucleic acids, where each

CC encoded protein contains a scaffold protein (e.g. a green fluorescent

CC protein - GFP) and a library peptide sequence comprising an alpha helical

CC biasing sequence, or a scaffold protein, a library peptide and a

CC nucleating sequence. The library of the invention is useful for screening

CC bioactive peptides conferring a particular phenotype. The present amino

CC acid sequence represents a scaffold protein.

XX Sequence 75 AA;

XX Query Match 60.0%; Score 63; DB 8; Length 75;

XX Best Local Similarity 66.7%; Pred. No. 0.42;

Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEAEKAKYAAAEAKAKAXA 25
: ||| ||| ||| ||| :
Db 4 DAAAEAAAKAAAEAAKAAAEAA 27

RESULT 32

ADK15665 ID ADK15665 standard; peptide; 75 AA.

AC ADK15665;

DT 06-MAY-2004 (first entry)

XX Nucleating sequence-containing library fusion protein #47.

XX fusion nucleic acid library; fusion protein library; scaffold protein;
KW green fluorescent protein; GFP; alpha helical biasing sequence;
XX nucleating sequence; screening.

OS Synthetic.

XX US2003224412-A1.

XX 04-DEC-2003.

PF 18-MAR-2003; 2003US-00393449.

PR 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

PR 20-JUN-2002; 2002US-00177725.

XX (ANDE/) ANDERSON D.

PA (PEEL/) PEELE B R.

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PI Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2004-033956/03.

XX Library of fusion polypeptides in which each polypeptides comprises

PT scaffold protein and library peptide having alpha helical biasing

PT sequence, or scaffold protein, library peptide and nucleating sequence.

XX Example 6; SEQ ID NO 53; 110pp; English.

XX The invention comprises a library of fusion nucleic acids, where each

CC encoded protein contains a scaffold protein (e.g. a green fluorescent

CC protein - GFP) and a library peptide sequence comprising an alpha helical

CC biasing sequence, or a scaffold protein, a library peptide and a

CC nucleating sequence. The library of the invention is useful for screening

CC bioactive peptides conferring a particular phenotype. The present amino

CC acid sequence represents a library protein containing a nucleating

XX Sequence 75 AA;

XX Query Match 60.0%; Score 63; DB 8; Length 75;

XX Best Local Similarity 66.7%; Pred. No. 0.42; Mismatches 6; Indels 0; Gaps 0;

RESULT 33

ADK10695 ID ADK10695 standard; protein; 83 AA.

AC ADK10695;

XX

DT 29-JAN-2004 (first entry)
 XX Structurally biased random peptide library scaffold protein seqid 102.
 DE
 XX fusion nucleic acid library; scaffold protein; bioactive peptide;
 KM phenotypic change; cell morphology; cell growth; cell viability;
 KM cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KM loss of cell division; decreased cell growth; brca-1; brca-2;
 KM tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KM Drosophila discs-large; Dig; cardiovascular; neurobiology; bone biology;
 KM skin biology; cosmetic; endocrinology; infectious disease;
 KM drug toxicity; drug resistance; inflammation; allergic response;
 KM scaffold protein.
 XX
 OS Synthetic.
 XX
 PN US2003143562-A1.
 PD
 XX 31-JUL-2003.
 PF 20-JUN-2002; 2002US-00177725.
 XX
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 XX
 PA (RIGEL-) RIGEL PHARM INC.
 PI Anderson D, Peelle BR, Bogenberger JM;
 XX WPI; 2003-829786/77.
 DR
 XX Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX
 PS Disclosure; SEQ ID NO 102; 110pp; English.
 XX
 CC The invention describes a library (1) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence,
 CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dig), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmetic applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a scaffold protein used in

CC peptide libraries or hold the library peptide in a conformationally
 CC restricted form.
 XX
 CC Sequence 83 AA;
 SQ
 Query Match 60.0%; Score 63; DB 7; Length 83;
 Best Local Similarity 66.7%; Pred. No. 0.47;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AKAARAKAKYAAAKAKAKX 24
 Db 57 AKAARAKAKAKAKAKAKAKAK 80
 RESULT 34
 ADE10645
 ID ADE10645 standard; protein; 83 AA.
 XX
 AC ADE10645;
 XX
 DT 29-JAN-2004 (first entry)
 DE
 XX Structurally biased random peptide library related protein seqid 52.
 DE
 KM fusion nucleic acid library; scaffold protein; bioactive peptide;
 KM phenotypic change; cell morphology; cell growth; cell viability;
 KM cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KM loss of cell division; decreased cell growth; brca-1; brca-2;
 KM tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KM Drosophila discs-large; Dig; cardiovascular; neurobiology; bone biology;
 KM skin biology; cosmetic; endocrinology; infectious disease;
 KM drug toxicity; drug resistance; inflammation; allergic response.
 KM
 OS Synthetic.
 XX
 PN US2003143562-A1.
 PD
 XX 31-JUL-2003.
 PF 20-JUN-2002; 2002US-00177725.
 XX
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 XX
 PA (RIGEL-) RIGEL PHARM INC.
 PI Anderson D, Peelle BR, Bogenberger JM;
 XX WPI; 2003-829786/77.
 DR
 XX Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX
 PS Example 6; SEQ ID NO 52; 110pp; English.
 XX
 CC The invention describes a library (1) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence,
 CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed

CC method is also useful in cancer applications. Random libraries can be
CC introduced into any tumour cell (primary or cultured), and peptides
CC identified which by themselves induce apoptosis, cell death, loss of cell
CC division or decreased cell growth. The method is also useful for
CC screening of bioactive peptides which restore the constitutive function
CC of the bcr-a-1 or bcr-a-2 genes, and other tumour suppressor genes
CC important in breast cancer such as the adenomatous polyposis coli gene
CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
CC cell-cell junctions. The methods are useful in cardiovascular
CC applications, neurobiology applications, bone biology applications, skin
CC biology applications, cosmetic applications, endocrinology
CC applications, infectious disease applications, drug toxicities and drug
CC resistance applications, immunobiology, inflammation, and allergic
CC response applications, and biotechnology applications. The peptide
CC library can easily be monitored, both for its presence within cells and
CC its quantity. The expression of structurally biased libraries generate
CC elevated cellular concentration of peptides having a given structural
CC bias and thus increase the hit rate for targets that bind such
CC structures. This is the amino acid sequence of a protein associated with
CC fused nucleic acid and random peptide libraries of the invention.

XX Sequence 83 AA;

Query Match 60.0%; Score 63; DB 7; Length 83;
Best Local Similarity 66.7%; Pred. No. 0.47;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAEAEKAKYAAAEAKAKAX 24
| : ||| ||| ||| ||| :
Db 57 AAKAAAEAAKAAAEAAKAAK 80

XX RESULT 35

ADK15714

ID ADK15714 standard; peptide; 83 AA.

XX ADK15714;

XX 06-MAY-2004 (first entry)

XX Library fusion protein-related scaffold protein #46.

XX fusion nucleic acid library; fusion protein library; scaffold protein;

XX green fluorescent protein; GFP; alpha helical biasing sequence;

XX nucleating sequence; screening.

XX Synthetic.

XX US2003224412-A1.

XX 04-DEC-2003.

XX 18-MAR-2003; 2003US-00393449.

XX 08-OCT-1998; 98US-00169015.

XX 08-OCT-1999; 99US-00415765.

XX 20-JUN-2002; 2002US-00177725.

XX (ANDE/) ANDERSON D.

XX (PEEL/) PELLIE B R.

XX (BOGE/) BOGENBERGER J M.

XX Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2004-033956/03.

PT Library of fusion polypeptides in which each polypeptide comprises
PT scaffold protein and library peptide having alpha helical biasing
PT sequence, or scaffold protein, library peptide and nucleating sequence.

XX Disclosure; SEQ ID NO 102; 110pp; English.

XX The invention comprises a library of fusion nucleic acids, where each

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CC protein - GFP) and a library peptide sequence comprising an alpha helical
CC biasing sequence, or a scaffold protein, a library peptide and a
CC nucleating sequence. The library of the invention is useful for screening
CC bioactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a scaffold protein.

XX Sequence 83 AA;

Query Match 60.0%; Score 63; DB 8; Length 83;
Best Local Similarity 66.7%; Pred. No. 0.47;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAEAEKAKYAAAEAKAKAX 24
| : ||| ||| ||| ||| :
Db 57 AAKAAAEAAKAAAEAAKAAK 80

XX RESULT 36

ADK15664

ID ADK15664 standard; peptide; 83 AA.

XX ADK15664;

XX 06-MAY-2004 (first entry)

XX Nucleating sequence-containing library fusion protein #46.

XX fusion nucleic acid library; fusion protein library; scaffold protein;

XX green fluorescent protein; GFP; alpha helical biasing sequence;

XX nucleating sequence; screening.

XX Synthetic.

XX US2003224412-A1.

XX 18-MAR-2003; 2003US-00393449.

XX 08-OCT-1998; 98US-00169015.

XX 08-OCT-1999; 99US-00415765.

XX 20-JUN-2002; 2002US-00177725.

XX (ANDE/) ANDERSON D.

XX (PEEL/) PELLIE B R.

XX (BOGE/) BOGENBERGER J M.

XX Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2004-033956/03.

PT Library of fusion polypeptides in which each polypeptide comprises
PT scaffold protein and library peptide having alpha helical biasing
PT sequence, or scaffold protein, library peptide and nucleating sequence.
XX Example 6; SEQ ID NO 52; 110pp; English.

CC The invention comprises a library of fusion nucleic acids, where each
CC encoded protein contains a scaffold protein (e.g. a green fluorescent
CC protein - GFP) and a library peptide sequence comprising an alpha helical
CC biasing sequence, or a scaffold protein, a library peptide and a
CC nucleating sequence. The library of the invention is useful for screening
CC bioactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a library protein containing a nucleating
CC sequence.

XX Sequence 83 AA;

Query Match 60.0%; Score 63; DB 8; Length 83;
Best Local Similarity 66.7%; Pred. No. 0.47;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAAAEKAKYAAEAEEKAKAX 24
|: ||| ||| ||| ||| |
Db 57 AAKAAAEAAAKAAAEAAAKAAAK 80

RESULT 37

ADBI0642
ID ADEI0642 standard; protein; 88 AA.

AC ADEI0642;

XX 29-JAN-2004 (first entry)

DE Structurally biased random peptide library related protein seqid 49.

KW fusion nucleic acid library; scaffold protein; bioactive peptide;
KW phenotype change; cell morphology; cell growth; cell viability;
KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KW loss of cell division; decreased cell growth; brca-1; brca-2;
KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KW Drosophila discs-large; Dig; cardiovascular; neurobiology; bone biology;
KW skin biology; cosmetic; endocrinology; infectious disease;
KW drug toxicity; drug resistance; inflammation; allergic response.

XX Synthetic.

OS US2003143562-A1.

PN 31-JUL-2003.

XX 20-JUN-2002; 2002US-00177725.

XX 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

XX (RIG-) RIGEL PHARM INC.

PI Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2003-829786/77.

PT Novel library of fusion nucleic acids each of which has fused first and
PT second nucleic acids encoding scaffold protein and library peptide having
PT alpha helical biasing sequence, respectively, useful in screening
PT methods.

XX Example 6; SEQ ID NO 49; 110pp; English.

CC The invention describes a library (1) of fusion nucleic acids, where each
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence, and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence;
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
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CC morphology, cell growth, cell viability, adhesion to substrates or other
CC cells, and cellular density; changes in the expression of one or more
CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
CC peptide identified by above mentioned method is used to generate more
CC candidate peptides and to identify target molecules, i.e., the molecules
CC with which the bioactive peptide interacts. The peptide(s) can be
CC combined with other pharmacologic activators to study the epistatic
CC relationships of signal transduction pathways in question. The disclosed
CC method is also useful in cancer applications. Random libraries can be
CC introduced into any tumour cell (primary or cultured), and peptides
CC identified which by themselves induce apoptosis, cell death, loss of cell
CC division or decreased cell growth. The method is also useful for
CC screening of bioactive peptides which restore the constitutive function
CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
CC important in breast cancer such as the adenomatous polyposis coli gene
CC (APC) and the Drosophila discs-large gene (Dig), which are components of
CC cell-cell junctions. The methods are useful in cardiovascular

CC applications, neurobiology applications, bone biology applications, skin
CC biology applications, cosmetic applications, endocrinology
CC applications, infectious disease applications, drug toxicities and drug
CC resistance applications, immunobiology, inflammation, and allergic
CC response applications, and biotechnology applications. The peptide
CC library can easily be monitored, both for its presence within cells and
CC its quantity. The expression of structurally biased libraries generate
CC elevated cellular concentration of peptides having a given structural
CC bias and thus increase the hit rate for targets that bind such
CC structures. This is the amino acid sequence of a protein associated with
CC fused nucleic acid and random peptide libraries of the invention.

XX Sequence 88 AA;

Query Match 60.0%; Score 63; DB 7; Length 88;

Best Local Similarity 66.7%; Pred. No. 0.5;

Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAAAEKAKYAAEAEEKAKAX 24
|: ||| ||| ||| ||| |
Db 63 AAKAAAEAAAKAAAEAAAKAAAK 86

RESULT 38

ADBI0692
ID ADEI0692 standard; protein; 88 AA.

AC ADEI0692;

XX 29-JAN-2004 (first entry)

DE Structurally biased random peptide library scaffold protein seqid 99.

KW fusion nucleic acid library; scaffold protein; bioactive peptide;
KW phenotype change; cell morphology; cell growth; cell viability;
KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KW loss of cell division; decreased cell growth; brca-1; brca-2;
KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KW Drosophila discs-large; Dig; cardiovascular; neurobiology; bone biology;
KW skin biology; cosmetic; endocrinology; infectious disease;
KW drug toxicity; drug resistance; inflammation; allergic response;
KW scaffold protein.

XX Synthetic.

OS US2003143562-A1.

PN 31-JUL-2003.

XX 20-JUN-2002; 2002US-00177725.

XX 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

XX (RIG-) RIGEL PHARM INC.

PI Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2003-829786/77.

PT Novel library of fusion nucleic acids each of which has fused first and
PT second nucleic acids encoding scaffold protein and library peptide having
PT alpha helical biasing sequence, respectively, useful in screening
PT methods.

XX Disclosure; SEQ ID NO 99; 110pp; English.

CC The invention describes a library (1) of fusion nucleic acids, where each
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence, and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence;
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
CC peptides conferring a change in specific phenotype such as cell

CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the bcr-a1 or bcr-a2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmetic applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a scaffold protein used in
 CC peptide libraries or hold the library peptide in a conformationally
 CC restricted form.

CC Sequence 88 AA;

Query Match 60.0%; Score 63; DB 7; Length 88;

Best Local Similarity 66.7%; Pred. No. 0.5;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AXAEAEKAAKAAAEAKAKAX 24
 : ||| ||| ||| ||| :
 Db 63 AAKAAAEAAKAAAEAAKAAKAAK 86

RESULT 39

ADK15711
 ID ADK15711 standard; peptide; 88 AA.

XX AC ADK15711;

DT 06-MAY-2004 (first entry)

XX DE Library fusion protein-related scaffold protein #43.

XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.

XX OS Synthetic.

XX PN US2003224412-A1.

XX PD 04-DEC-2003.

PF 18-MAR-2003; 2003US-00393449.

PR 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

PR 20-JUN-2002; 2002US-00177725.

XX PA (ANDE/) ANDERSON D.
 PA (PEEL/) PELLIE B R.
 PA (BOGE/) BOGENBERGER J M.

PI Anderson D, Peelle BR, Bogenberger JM;
 XX WPI; 2004-033956/03.
 XX PT Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.
 XX PS Disclosure; SEQ ID NO 99; 110pp; English.

XX CC The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a
 CC nucleating sequence. The library of the invention is useful for screening
 CC bioactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a scaffold protein.

XX Sequence 88 AA;

Query Match 60.0%; Score 63; DB 8; Length 88;

Best Local Similarity 66.7%; Pred. No. 0.5;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AXAEAEKAAKAAAEAKAKAX 24
 : ||| ||| ||| ||| :
 Db 63 AAKAAAEAAKAAAEAAKAAKAAK 86

RESULT 40
 ADK15661
 ID ADK15661 standard; peptide; 88 AA.

XX AC ADK15661;

DT 06-MAY-2004 (first entry)

XX DE Nucleating sequence-containing library fusion protein #43.

XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.

XX OS Synthetic.

XX PN US2003224412-A1.

XX PD 04-DEC-2003.

PF 18-MAR-2003; 2003US-00393449.

PR 08-OCT-1998; 98US-00169015.

PR 08-OCT-1999; 99US-00415765.

PR 20-JUN-2002; 2002US-00177725.

XX PA (ANDE/) ANDERSON D.
 PA (PEEL/) PELLIE B R.
 PA (BOGE/) BOGENBERGER J M.

XX PI Anderson D, Peelle BR, Bogenberger JM;

XX DR WPI; 2004-033956/03.

XX PT Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.

XX PS Example 6; SEQ ID NO 49; 110pp; English.

XX CC The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a

CC nucleating sequence. The library of the invention is useful for screening
CC bioactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a library protein containing a nucleating
CC sequence.
XX
SQ Sequence 88 AA;
Query Match 60.0%; Score 63; DB 8; Length 88;
Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
DY 1 AXAAEAERKAKYAAEAERKAKAX 24
Db 63 AAKXAAEAERKAKYAAEAERKAKAX 86
RESULT 41
ADE10694
ID ADE10694 standard; protein; 91 AA.
XX
AC ADE10694;
XX
DT 29-JAN-2004 (first entry)
XX
DE Structurally biased random peptide library scaffold protein seqid 101.
XX
KM fusion nucleic acid library; scaffold protein; bioactive peptide;
KM phenotype change; cell morphology; cell growth; cell viability;
KM cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KM loss of cell division; decreased cell growth; brca-1; brca-2;
KM tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KM Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
KM skin biology; cosmetic; endocrinology; infectious disease;
KM drug toxicity; drug resistance; inflammation; allergic response;
KM scaffold protein.
XX
OS Synthetic.
XX
PN US2003143562-A1.
XX
PD 31-JUL-2003.
XX
PF 20-JUN-2002; 2002US-00177725.
XX
PR 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
XX
PA (RIGE-) RIGEL PHARM INC.
PI Anderson D, Peelle BR, Bogenberger JM;
XX
DR WPI; 2003-829786/77.
XX
PT Novel library of fusion nucleic acids each of which has fused first and
PT second nucleic acids encoding scaffold protein and library peptide having
PT alpha helical biasing sequence, respectively, useful in screening
PT methods.
PS
XX Disclosure; SEQ ID NO 101; 110pp; English.
XX
CC The invention describes a library (1) of fusion nucleic acids, where each
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence;
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
CC peptides conferring a change in specific phenotype such as cell
CC morphology, cell growth, cell viability, adhesion to substrates or other
CC cells, and cellular density; changes in the expression of one or more
CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
CC peptide identified by above mentioned method is used to generate more
CC candidate peptides and to identify target molecules, i.e., the molecules

CC with which the bioactive peptide interacts. The peptide(s) can be
CC combined with other pharmacologic activators to study the epistatic
CC relationships of signal transduction pathways in question. The disclosed
CC method is also useful in cancer applications. Random libraries can be
CC introduced into any tumour cell (primary or cultured), and peptides
CC identified which by themselves induce apoptosis, cell death, loss of cell
CC division or decreased cell growth. The method is also useful for
CC screening of bioactive peptides which restore the constitutive function
CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
CC important in breast cancer such as the adenomatous polyposis coli gene
CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
CC cell-cell junctions. The methods are useful in cardiovascular
CC applications, neurobiology applications, bone biology applications, skin
CC biology applications, infectious disease applications, endocrinology
CC applications, cosmetic applications, drug toxicities and drug
CC resistance applications, immunobiology, inflammation, and allergic
CC response applications, and biotechnology applications. The peptide
CC library can easily be monitored, both for its presence within cells and
CC its quantity. The expression of structurally biased libraries generate
CC elevated cellular concentration of peptides having a given structural
CC bias and thus increase the hit rate for targets that bind such
CC structures. This is the amino acid sequence of a scaffold protein used in
CC peptide libraries to hold the library peptide in a conformationally
CC restricted form.
XX
SQ Sequence 91 AA;
Query Match 60.0%; Score 63; DB 7; Length 91;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
DY 1 AXAAEAERKAKYAAEAERKAKAX 24
Db 65 AAKXAAEAERKAKYAAEAERKAKAX 88
RESULT 42
ADE10644
ID ADE10644 standard; protein; 91 AA.
XX
AC ADE10644;
XX
DT 29-JAN-2004 (first entry)
XX
DE Structurally biased random peptide library related protein seqid 51.
XX
KM fusion nucleic acid library; scaffold protein; bioactive peptide;
KM phenotype change; cell morphology; cell growth; cell viability;
KM cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KM loss of cell division; decreased cell growth; brca-1; brca-2;
KM tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KM Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
KM skin biology; cosmetic; endocrinology; infectious disease;
KM drug toxicity; drug resistance; inflammation; allergic response.
XX
OS Synthetic.
XX
PN US2003143562-A1.
XX
PD 31-JUL-2003.
XX
PF 20-JUN-2002; 2002US-00177725.
XX
PR 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
XX
PA (RIGE-) RIGEL PHARM INC.
PI Anderson D, Peelle BR, Bogenberger JM;
XX
DR WPI; 2003-829786/77.
XX
PT Novel library of fusion nucleic acids each of which has fused first and

PT second nucleic acids encoding scaffold protein and library peptide having
PT alpha helical biasing sequence, respectively, useful in screening
PT methods.

Example 6; SEQ ID NO 51; 110pp; English.

CC The invention describes a library (I) of fusion nucleic acids, where each
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence;
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
CC peptides conferring a change in specific phenotype such as cell
CC morphology, cell growth, cell viability, adhesion to substrates or other
CC cells, and cellular density; changes in the expression of one or more
CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
CC peptide identified by above mentioned method is used to generate more
CC candidate peptides and to identify target molecules, i.e., the molecules
CC with which the bioactive peptide interacts. The peptide(s) can be
CC combined with other pharmacologic activators to study the epistatic
CC relationships of signal transduction pathways in question. The disclosed
CC method is also useful in cancer applications. Random libraries can be
CC introduced into any tumour cell (primary or cultured), and peptides
CC identified which by themselves induce apoptosis, cell death, loss of cell
CC division or decreased cell growth. The method is also useful for
CC screening of bioactive peptides which restore the constitutive function
CC of the bcr-a1 or bcr-a2 genes, and other tumour suppressor genes
CC important in breast cancer such as the adenomatous polyposis coli gene
CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
CC cell-cell junctions. The methods are useful in cardiovascular
CC applications, neurobiology applications, bone biology applications, skin
CC biology applications, cosmetic applications, endocrinology
CC applications, infectious disease applications, drug toxicities and drug
CC resistance applications, immunobiology, inflammation, and allergic
CC response applications, and biotechnology applications. The peptide
CC library can easily be monitored, both for its presence within cells and
CC its quantity. The expression of structurally biased libraries generate
CC elevated cellular concentration of peptides having a given structural
CC bias and thus increase the hit rate for targets that bind such
CC structures. This is the amino acid sequence of a protein associated with
CC fused nucleic acid and random peptide libraries of the invention.

CC XX Sequence 91 AA;

Query Match 60.0%; Score 63; DB 7; Length 91;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAEEAERAKYAAAEAKAKAX 24
Db 65 AAKAAAEAAAKAAAEAAAKAAAK 88

RESULT 43
ADK15663
ID ADK15663 standard; peptide; 91 AA.

XX AC ADK15663;

XX DT 06-MAY-2004 (first entry)

XX DE Nucleating sequence-containing library fusion protein #45.

XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
KW green fluorescent protein; GFP; alpha helical biasing sequence;
KW nucleating sequence; screening.

XX OS Synthetic.

XX PN US2003224412-A1.

XX PD 04-DEC-2003.

XX 18-MAR-2003; 2003US-00393449.

XX PF 08-OCT-1998; 98US-00169015.

XX PR 08-OCT-1999; 99US-00415765.

XX PR 20-JUN-2002; 2002US-00177725.

XX PA (ANDE/) ANDERSON D.

XX PA (PEEL/) PELLE B R.

XX PA (BOGE/) BOGENBERGER J M.

XX PI Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2004-033956/03.

XX DR WPI; 2004-033956/03.

XX PT Library of fusion polypeptides in which each polypeptides comprises

XX PT scaffold protein and library peptide having alpha helical biasing

XX PT sequence, or scaffold protein, library peptide and nucleating sequence.

XX PS Example 6; SEQ ID NO 51; 110pp; English.

XX CC The invention comprises a library of fusion nucleic acids, where each

XX CC encoded protein contains a scaffold protein (e.g. a green fluorescent

XX CC protein - GFP) and a library peptide sequence comprising an alpha helical

XX CC biasing sequence, or a scaffold protein, a library peptide and a

XX CC nucleating sequence. The library of the invention is useful for screening

XX CC bioactive peptides conferring a particular phenotype. The present amino

XX CC acid sequence represents a library protein containing a nucleating

XX CC sequence.

XX SQ Sequence 91 AA;

Query Match 60.0%; Score 63; DB 8; Length 91;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAEEAERAKYAAAEAKAKAX 24
Db 65 AAKAAAEAAAKAAAEAAAKAAAK 88

RESULT 44
ADK15713
ID ADK15713 standard; peptide; 91 AA.

XX AC ADK15713;

XX DT 06-MAY-2004 (first entry)

XX DE Library fusion protein-related scaffold protein #45.

XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
KW green fluorescent protein; GFP; alpha helical biasing sequence;
KW nucleating sequence; screening.

XX OS Synthetic.

XX PN US2003224412-A1.

XX PD 04-DEC-2003.

XX PF 18-MAR-2003; 2003US-00393449.

XX PR 08-OCT-1998; 98US-00169015.

XX PR 08-OCT-1999; 99US-00415765.

XX PR 20-JUN-2002; 2002US-00177725.

XX PA (ANDE/) ANDERSON D.

XX PA (PEEL/) PELLE B R.

XX PA (BOGE/) BOGENBERGER J M.

XX PI Anderson D, Peelle BR, Bogenberger JM;

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OM protein - protein search, using sw model

Run on: July 11, 2005, 09:37:04 ; Search time 42 Seconds
(without alignments)
44.434 Million cell updates/sec

Title: SEQ1
Perfect score: 105
Sequence: 1 axaaeakakyaakaaakakaxa 25

Scoring table:
BIOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	64.8	69	US-09-902-540-14824	Sequence 14824, A
2	61.5	58.6	56	US-09-405-743A-3	Sequence 3, Appli
3	61.5	58.6	56	US-09-816-989A-3	Sequence 3, Appli
4	61.5	58.6	86	US-09-405-743A-6	Sequence 6, Appli
5	61.5	58.6	86	US-09-816-989A-6	Sequence 6, Appli
6	61	58.1	33	US-08-303-025-16	Sequence 16, Appli
7	61	58.1	33	US-08-436-703B-4	Sequence 4, Appli
8	61	58.1	469	US-09-489-039A-13565	Sequence 13565, A
9	60.5	57.6	117	US-09-340-736E-9	Sequence 9, Appli
10	60.5	57.6	117	US-09-964-662-9	Sequence 9, Appli
11	60.5	57.6	118	US-09-340-736E-10	Sequence 10, Appli
12	60.5	57.6	118	US-09-964-662-10	Sequence 10, Appli
13	60.5	57.6	199	US-09-340-736E-11	Sequence 11, Appli
14	60.5	57.6	199	US-09-964-662-11	Sequence 11, Appli
15	60.5	57.6	200	US-09-340-736E-2	Sequence 2, Appli
16	60.5	57.6	200	US-09-964-662-2	Sequence 2, Appli
17	60.5	57.6	201	US-08-911-364-2	Sequence 2, Appli
18	60.5	57.6	730	US-09-961-403-8	Sequence 8, Appli
19	60.5	57.6	731	US-08-911-364-1	Sequence 1, Appli
20	60.5	57.6	731	US-09-340-736E-1	Sequence 1, Appli
21	60.5	57.6	731	US-09-964-662-1	Sequence 1, Appli
22	60.5	57.6	733	US-08-464-700-2	Sequence 2, Appli
23	60.5	57.6	733	US-09-869-875-7	Sequence 7, Appli
24	59	56.2	45	US-09-405-743A-2	Sequence 2, Appli
25	59	56.2	45	US-09-816-989A-2	Sequence 2, Appli
26	59	56.2	109	US-09-405-743A-7	Sequence 7, Appli
27	59	56.2	109	US-09-816-989A-7	Sequence 7, Appli

28	58	55.2	77	4	US-09-405-743A-5	Sequence 5, Appli
29	58	55.2	77	4	US-09-816-989A-5	Sequence 5, Appli
30	58	55.2	92	4	US-09-344-529-2	Sequence 2, Appli
31	57.5	54.8	325	4	US-09-902-540-13678	Sequence 13678, A
32	57	54.3	28	1	US-08-303-025-12	Sequence 12, Appli
33	57	54.3	28	2	US-08-436-703B-1	Sequence 1, Appli
34	57	54.3	29	1	US-08-152-488-10	Sequence 10, Appli
35	57	54.3	29	1	US-08-152-488-11	Sequence 11, Appli
36	57	54.3	29	1	US-08-152-488-12	Sequence 12, Appli
37	57	54.3	29	1	US-08-303-025-10	Sequence 10, Appli
38	57	54.3	29	1	US-08-303-025-11	Sequence 11, Appli
39	57	54.3	29	1	US-08-303-025-13	Sequence 13, Appli
40	57	54.3	29	1	US-08-303-025-14	Sequence 14, Appli
41	57	54.3	29	1	US-08-677-304-10	Sequence 10, Appli
42	57	54.3	29	1	US-08-677-304-11	Sequence 11, Appli
43	57	54.3	29	1	US-08-677-304-12	Sequence 12, Appli
44	57	54.3	29	2	US-08-436-703B-3	Sequence 3, Appli
45	57	54.3	29	2	US-08-436-703B-15	Sequence 15, Appli

ALIGNMENTS

```
RESULT 1
US-09-902-540-14824
; Sequence 14824, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14824
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14824

Query Match      64.8%; Score 68; DB 4; Length 69;
Best Local Similarity 64.0%; Pred. No. 0.018;
Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Cy      1 AXAAEAKAKYAAEAKAKAKXA 25
Db      12 AAKRAAEAAKRAAEARRAEEAAA 36

RESULT 2
US-09-405-743A-3
; Sequence 3, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
```

US-09-405-743A-3

Query Match 58.6%; Score 61.5; DB 4; Length 56;
Best Local Similarity 64.0%; Pred. No. 0.1;
Matches 16; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 2 XAEAEKA-AKYAAEAKAKAXA 25
Db 29 AAEKKKAEEAKYKAAKAAKAAKAA 53

RESULT 3

US-09-816-989A-3
Sequence 3, Application US/09816989A
Patent No. 6800287
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23, 693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3

Query Match 58.6%; Score 61.5; DB 4; Length 56;
Best Local Similarity 64.0%; Pred. No. 0.1;
Matches 16; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 2 XAEAEKA-AKYAAEAKAKAXA 25
Db 29 AAEKKKAEEAKYKAAKAAKAAKAA 53

RESULT 4

US-09-405-743A-6
Sequence 6, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 86
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
OTHER INFORMATION: PEPTIDE
US-09-405-743A-6

Query Match 58.6%; Score 61.5; DB 4; Length 86;
Best Local Similarity 60.7%; Pred. No. 0.17;
Matches 17; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 1 AXAEAEKA-AKYAAEAKAKAXA 25
Db 17 AAEKKKAEEAKYKAAKAAKAAKAA 53

Db 47 AKAEEKAAAEAKYKAAKAKYKAA 74

RESULT 5

US-09-816-989A-6
Sequence 6, Application US/09816989A
Patent No. 6800287
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23, 693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 86
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6

Query Match 58.6%; Score 61.5; DB 4; Length 86;
Best Local Similarity 60.7%; Pred. No. 0.17;
Matches 17; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 1 AXAEAEKA-AKYAAEAKAKAXA 25
Db 47 AKAEEKAAAEAKYKAAKAKYKAA 74

RESULT 6

US-08-303-025-16
Sequence 16, Application US/08303025
Patent No. 561494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.

REFERENCE/DOCKET NUMBER: 7WH-060548-00231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-303-025-16

Query Match 58.1%; Score 61; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 0.067;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 EAAEKAAKYAAEAERAKAKAX 24
DB 1 EAAKKAARKAKAKAKAKAKAA 21

RESULT 7
US-08-436-703B-4
Sequence 4, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Benita J. Rohm, Esq.
STREET: 6601 Woodward Avenue
CITY: Suite 1525
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6;
SOFTWARE: ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-00233
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids

TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
US-08-436-703B-4

Query Match 58.1%; Score 61; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 0.067;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 EAAEKAAKYAAEAERAKAKAX 24
DB 1 EAAKKAARKAKAKAKAKAKAA 21

RESULT 8
US-09-489-039A-13565
Sequence 9, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
LENGTH: 469
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13565

Query Match 58.1%; Score 61; DB 4; Length 469;
Best Local Similarity 62.5%; Pred. No. 1.3;
Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEEAERAKAYAAEAERAKAKAX 25
DB 301 KAABAERAKAAADUKAKAKAA 324

RESULT 9
US-09-340-736E-9
Sequence 9, Application US/09340736E
Patent No. 6489446
GENERAL INFORMATION:
APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELEY, FRED
APPLICANT: ROTHSTEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: MFU-3 polypeptide
US-09-340-736E-9

Query Match 57.6%; Score 60.5; DB 4; Length 117;
Best Local Similarity 58.6%; Pred. No. 0.32;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 AXAAAEKAKY-----AAEAERKAKX 24
Db 37 AQAATAAKAKYGVGTPRAAAAKAAKAA 65

RESULT 10
US-09-964-662-9
Sequence 9, Application US/09964662
Patent No. 6765086
GENERAL INFORMATION:
APPLICANT: PROTEIN SPECIALTIES LTD.
APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
FILE REFERENCE: 041082/0112
CURRENT APPLICATION NUMBER: US/09/964,662
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: 09/340,736
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-662-9

Query Match 57.6%; Score 60.5; DB 4; Length 117;
Best Local Similarity 58.6%; Pred. No. 0.32;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 AXAAAEKAKY-----AAEAERKAKX 24
Db 37 AQAATAAKAKYGVGTPRAAAAKAAKAA 65

RESULT 11
US-09-340-736E-10
Sequence 10, Application US/09340736E
Patent No. 6489446
GENERAL INFORMATION:
APPLICANT: KOTHEIN, ASER
APPLICANT: KOTHEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: MFU-4 polypeptide
US-09-340-736E-10

Query Match 57.6%; Score 60.5; DB 4; Length 118;

Best Local Similarity 58.6%; Pred. No. 0.33;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 AXAAAEKAKY-----AAEAERKAKX 24
Db 38 AQAATAAKAKYGVGTPRAAAAKAAKAA 66

RESULT 12
US-09-964-662-10
Sequence 10, Application US/09964662
Patent No. 6765086
GENERAL INFORMATION:
APPLICANT: PROTEIN SPECIALTIES LTD.
APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
FILE REFERENCE: 041082/0112
CURRENT APPLICATION NUMBER: US/09/964,662
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: 09/340,736
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-662-10

Query Match 57.6%; Score 60.5; DB 4; Length 118;
Best Local Similarity 58.6%; Pred. No. 0.33;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 AXAAAEKAKY-----AAEAERKAKX 24
Db 38 AQAATAAKAKYGVGTPRAAAAKAAKAA 66

RESULT 13
US-09-340-736E-11
Sequence 11, Application US/09340736E
Patent No. 6489446
GENERAL INFORMATION:
APPLICANT: KOTHEIN, ASER
APPLICANT: KOTHEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 199
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: MFU-5 polypeptide
US-09-340-736E-11

Query Match 57.6%; Score 60.5; DB 4; Length 199;
Best Local Similarity 58.6%; Pred. No. 0.59;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 AXAAAEKAKY-----AAEAERKAKX 24

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-364-2

Query Match 57.6%; Score 60.5; DB 2; Length 201;
Best Local Similarity 58.6%; Pred. No. 0.6;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

Qy 1 AXAAAEKAKY-----AAEAERAKAX 24
Db 38 AQAATAAKAKYGVGTAPAAAAAKAAKAA 66

RESULT 18
US-09-961-403-8
Sequence 8, Application US/09961403
Patent No. 6780594
GENERAL INFORMATION:
APPLICANT: HE-STUMP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: RESIDOR, PEDRO
APPLICANT: SCOTT, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 730
TYPE: PRT
ORGANISM: Homo sapiens
US-09-961-403-8

Query Match 57.6%; Score 60.5; DB 4; Length 730;
Best Local Similarity 58.6%; Pred. No. 2.5;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

Qy 1 AXAAAEKAKY-----AAEAERAKAX 24
Db 441 AQAATAAKAKYGVGTAPAAAAAKAAKAA 469

RESULT 19
US-08-911-364-1
Sequence 1, Application US/08911364
Patent No. 5969106
GENERAL INFORMATION:
APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELIX, FRED W.
APPLICANT: ROTHSTEIN, STEVEN J.
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELLED ON HUMAN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,364
FILING DATE: 07-AUG-1997

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,552
FILING DATE: 07-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 041082/0104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-364-1

Query Match 57.6%; Score 60.5; DB 2; Length 731;
Best Local Similarity 58.6%; Pred. No. 2.5;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

Qy 1 AXAAAEKAKY-----AAEAERAKAX 24
Db 415 AQAATAAKAKYGVGTAPAAAAAKAAKAA 443

RESULT 20
US-09-340-736E-1
Sequence 1, Application US/09340736E
Patent No. 6489446
GENERAL INFORMATION:
APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELIX, FRED
APPLICANT: ROTHSTEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELLED ON HUMAN ELASTIN
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
PRIORITY FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIORITY FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIORITY FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 731
TYPE: PRT
ORGANISM: Homo sapiens
US-09-340-736E-1

Query Match 57.6%; Score 60.5; DB 4; Length 731;
Best Local Similarity 58.6%; Pred. No. 2.5;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

Qy 1 AXAAAEKAKY-----AAEAERAKAX 24
Db 415 AQAATAAKAKYGVGTAPAAAAAKAAKAA 443

RESULT 21
US-09-964-662-1
Sequence 1, Application US/09964662
Patent No. 6765086
GENERAL INFORMATION:
APPLICANT: PROTEIN SPECIALTIES LTD.
APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELLED ON HUMAN ELASTIN AND
FILE REFERENCE: 041082/0112

;; CURRENT APPLICATION NUMBER: US/09/964,662
;; CURRENT FILING DATE: 2003-05-08
;; PRIOR APPLICATION NUMBER: 09/340,736
;; PRIOR FILING DATE: 1999-06-29
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 731
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-964-662-1

Query Match 57.6%; Score 60.5; DB 4; Length 731;
Best Local Similarity 58.6%; Pred. No. 2.5;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 AAEEAEKAAKY-----AAEEAEKAAKX 24
Db 415 AAAAAAAKAAKYGVTPAAAAKAAKAA 443

RESULT 22
US-08-464-700-2
; Sequence 2, Application US/08464700
; Patent No. 6232458
; GENERAL INFORMATION:
; APPLICANT: WEISS, ANTHONY S
; APPLICANT: MARTIN, STEPHEN L
; TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,700
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL6520
; FILING DATE: 22-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL9661
; FILING DATE: 28-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU93/00655
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Maury E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GHC3USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 733 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-700-2

Query Match 57.6%; Score 60.5; DB 3; Length 733;
Best Local Similarity 58.6%; Pred. No. 2.6;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 AAEEAEKAAKY-----AAEEAEKAAKX 24
Db 417 AAAAAAAKAAKYGVTPAAAAKAAKAA 445

RESULT 23
US-09-869-875-7
; Sequence 7, Application US/09869875
; Patent No. 6521456
; GENERAL INFORMATION:
; APPLICANT: Siebenkotten, Gregor
; APPLICANT: Christine, Rainer
; TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC ACI
; TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE
; FILE REFERENCE: 30430.1USWO
; CURRENT APPLICATION NUMBER: US/09/869,875
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: PCT/DE00/00061
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: DE 199 00 513.3
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: DE 199 33 939.2
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA-NLS
US-09-869-875-7

Query Match 56.7%; Score 59.5; DB 4; Length 67;
Best Local Similarity 61.5%; Pred. No. 0.24;
Matches 16; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 AAEEAEKAAKYAA-EAEEKAAKXXA 25
Db 4 AAEEAEKAAKEAAEEAEKAAEEA 29

RESULT 24
US-09-405-743A-2
; Sequence 2, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-2

Query Match 56.2%; Score 59; DB 4; Length 45;
Best Local Similarity 58.3%; Pred. No. 0.18;
Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 XAEEAEKAAKYAAEEAEKAAKXXA 25
Db 18 KAAEAKKAAKYKAAEEKAAKAAKEA 41

RESULT 25
US-09-816-989A-2
; Sequence 2, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2

Query Match 56.2%; Score 59; DB 4; Length 45;
Best Local Similarity 58.3%; Pred. No. 0.18;
Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 XAEEAEKAKYAAEAEKAKAKA 25
Db 18 KAEEAKKAAKYEKAAEAEKAKA 41

RESULT 26
US-09-405-743A-7
; Sequence 7, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-405-743A-7

Query Match 56.2%; Score 59; DB 4; Length 109;
Best Local Similarity 56.0%; Pred. No. 0.47;
Matches 14; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 AXAEAEKAKYAAEAEKAKAKA 25
Db 82 AEAKKAEAKAKYKAEAKKAAKAKA 106

RESULT 27
US-09-816-989A-7
; Sequence 7, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-7

Query Match 56.2%; Score 59; DB 4; Length 109;
Best Local Similarity 56.0%; Pred. No. 0.47;
Matches 14; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 AXAEAEKAKYAAEAEKAKAKA 25
Db 82 AEAKKAEAKAKYKAEAKKAAKAKA 106

RESULT 28
US-09-405-743A-5
; Sequence 5, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-405-743A-5

Query Match 55.2%; Score 58; DB 4; Length 77;
Best Local Similarity 51.6%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

OY 1 AXAEAEKAKK-----YAEAEKAKAKA 25
Db 10 AYAKKAEKAKAKAEAKAKYKAEAKKAKA 40

RESULT 29
US-09-816-989A-5
; Sequence 5, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent version 3.1
SEQ ID NO 5
LENGTH: 77
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5

Query Match 55.2%; Score 58; DB 4; Length 77;
Best Local Similarity 51.6%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

Qy 1 AXAAAEKAAK-----YAAAEKAAKAXA 25
Db 10 AYAKKAERAAKAAKAYKAAAEKAAKAAEA 40

RESULT 30
US-09-344-529-2
Sequence 2, Application US/09344529
Patent No. 6429293
GENERAL INFORMATION:
APPLICANT: Hew, Choy L.
TITLE OF INVENTION: Sculptin-Type Antifreeze Polypeptides and Nucleic Acids
FILE REFERENCE: 016252-002620US
CURRENT APPLICATION NUMBER: US/09/344,529
CURRENT FILING DATE: 1999-06-24
EARLIER APPLICATION NUMBER: US 60/090,794
EARLIER FILING DATE: 1998-06-26
EARLIER APPLICATION NUMBER: US 60/095,713
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 2
LENGTH: 92
TYPE: PRT
ORGANISM: Myoxocephalus scorpius
US-09-344-529-2

Query Match 55.2%; Score 58; DB 4; Length 92;
Best Local Similarity 60.0%; Pred. No. 0.53;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AXAAAEKAAKAYAAAEKAAKAXA 25
Db 3 AAARAAEAAMAAANAAATXAA 27

RESULT 31
US-09-902-540-13678
Sequence 13678, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(115849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13678
LENGTH: 325
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-13678

Query Match 54.8%; Score 57.5; DB 4; Length 325;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches 16; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 AXAAAEKAAKAYAAEAAEKAAKAXA 25
Db 20 AAARAAEAAMAAANAAATXAA 45

RESULT 32
US-08-303-025-12
Sequence 12, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 7MH-060548-00231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-303-025-12

Query Match 54.3%; Score 57; DB 1; Length 28;
Best Local Similarity 56.5%; Pred. No. 0.19;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 XAAAEKAAKAYAAAEKAAKAXA 24
Db 1 PAKKAAKAAKAAKAAKAAKAAKAA 23

```

RESULT 33
US-08-436-703B-1
; Sequence 1, Application US/08436703B
; Patent No. 5919761
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR
; HEPARIN AND LOW MOLECULAR
; WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 6601 Woodward Avenue
; STREET: Suite 1525
; CITY: Detroit
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48226
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 1.44mb, 3.5"
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6;
; SOFTWARE: ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US//08/436,703B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: 7WK-060548-00233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313-965-1976
; TELEFAX: 313-965-1951
; INFORMATION FOR SEQ ID NO: 1 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
;
US-08-436-703B-1
Query Match 54.3%; Score 57; DB 2; Length 28;
Best Local Similarity 56.5%; Pred.No. 0.19;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      2 XAEAAEKRAKRAEAERKAACX 24
       |:|:||||| |:|:|||||
Db      1 PAKKAKKAKKAKKAKKAKKAA 23

RESULT 34
US-08-152-488-10
; Sequence 10, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
```

```

1 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
2 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
3 NUMBER OF SEQUENCES: 13
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Benita J. Rohm, Esq.
6 STREET: 512 Springfield Avenue
7 CITY: Cranford
8 STATE: New Jersey
9 COUNTRY: United States of America
10 ZIP: 07016-1811
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: MS-DOS
15 SOFTWARE: Wordperfect 6; ASCII (DOS)Text
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/152,488
18 FILING DATE: 12-NOV-1993
19 CLASSIFICATION: 514
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: PCT/US92/08069
22 FILING DATE: 14-AUG-1993
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Rohm, Benita J.
25 REGISTRATION NUMBER: 28,664
26 REFERENCE/DOCKET NUMBER: RM-7WG
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 908-276-3344
29 TELEFAX: 908-276-5543
30 INFORMATION FOR SEQ ID NO: 10:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 29 amino acids
33 TYPE: amino acid
34 STRANDEDNESS: N/A
35 TOPOLOGY: N/A
36 MOLECULE TYPE: peptide
37 ORIGINAL SOURCE:
38 ORGANISM: N/A
39 PUBLICATION INFORMATION:
40 AUTHORS: N/A
41 TITLE: N/A
42 PUBLICATION INFORMATION:
43 DOCUMENT NUMBER: PCT/US92/08069
44 FILING DATE: 14-AUG-1993
45 US-08-152-488-10
46
47 Query Match 54.3%; Score 57; DB 1; Length 29;
48 Best Local Similarity 56.5%; Pred. No. 0.2;
49 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
50
51 QY 2 XAEEAEKAKKYAAEAEKAKAX 24
52 :|:|||||:|||||:
53 Db 5 AAKKAKKKAKKAKKAAKAKKAAA 27
54
55 RESULT 35
56 US-08-152-488-11
57 Sequence 11, Application US/08152488
58 Patent No. 5534619
59 GENERAL INFORMATION:
60 APPLICANT: Wakefield, Thomas W.
61 APPLICANT: Andrews, Philip C.
62 APPLICANT: Stanley, James C.
63 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
64 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
65 TITLE OF INVENTION: ANTI COAGULATION REVERSAL
66 NUMBER OF SEQUENCES: 13
67 CORRESPONDENCE ADDRESS:
68 ADDRESSEE: Benita J. Rohm, Esq.
69 STREET: 512 Springfield Avenue
70 CITY: Cranford
71 STATE: New Jersey
72 COUNTRY: United States of America

```

ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-11

Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

CY 2 XABAERAKYAAEAERAKAX 24
Db 5 AAKAKAKAKAKAKAKAKAKA 27

RESULT 36
US-08-152-488-12
Sequence 12, Application US/08152488
Patent No. 5534619
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-12

Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

CY 2 XABAERAKYAAEAERAKAX 24
Db 5 AAKAKAKAKAKAKAKAKAKA 27

RESULT 37
US-08-303-025-10
Sequence 10, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231

TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-303-025-10

Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Oy 2 XAENAEKAKYAAAEKAKAX 24
Db 5 AAKKAKKAKKAKKAKKAKKAA 27

RESULT 38

US-08-303-025-11
Sequence 11, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: Wordperfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-303-025-11

Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Oy 2 XAENAEKAKYAAAEKAKAX 24
Db 5 AAKKAKKAKKAKKAKKAKKAA 27

RESULT 39

US-08-303-025-13
Sequence 13, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: Wordperfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-303-025-13

Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 XAAEAERAKKAAEAERAKKAX 24
DB 5 AAKKAKKAAKKAKKAKKAKKAA 27

RESULT 40
US-08-303-025-14
; Sequence 14, Application US/08303025
; Patent No. 5614494
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 150 West Jefferson, Suite 2500
; CITY: Detroit
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48226-4415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette 3.5" 1.44MB
; OPERATING SYSTEM: MS-DOS V.6.22
; SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,025
; FILING DATE: 08-SEPT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06829
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: US 08/152,488
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 7MH-060548-00231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313-496-7622
; TELEFAX: 313-496-8454
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; US-08-303-025-14

Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 XAAEAERAKKAAEAERAKKAX 24
DB 5 AAKKAKKAAKKAKKAKKAKKAX 27

RESULT 41
US-08-677-304-10
; Sequence 10, Application US/08677304
; Patent No. 5721212
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,304
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: RM-7WG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 5721212 Relevant
; TOPOLOGY: No. 5721212 Relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; US-08-677-304-10

Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 XAAEAERAKKAAEAERAKKAX 24
DB 5 AAKKAKKAAKKAKKAKKAKKAA 27

RESULT 42
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; Sequence 11, Application US/08677304
; Patent No. 5721212
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.

APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-677-304-11
Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
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Db 5 AAKKAKKAKKAKKAKKAKKAKA 27
RESULT 43
US-08-677-304-12
Sequence 12, Application US/08677304
Patent No. 5721212
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-677-304-12
Query Match 54.3%; Score 57; DB 1; Length 29;
Best Local Similarity 56.5%; Pred. No. 0.2;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 2 XAENAEKAKYAAEAEKAKAX 24
Db 5 AAKKAKKAKKAKKAKKAKKAKA 27
RESULT 44
US-08-436-703B-3
Sequence 3, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 6601 Woodward Avenue
CITY: Suite 1525
STATE: Michigan
COUNTRY: United States of America

ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6/
SOFTWARE: ASCII (DOS)text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-00233
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
; JS-08-436-703B-3

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      FILING DATE: 08-MAY-1995
      CLASSIFICATION: 514
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      APPLICATION NUMBER: N/A
      FILING DATE: N/A
      ATTORNEY/AGENT INFORMATION:
      NAME: Rohm, Benita J.
      REGISTRATION NUMBER: 28,664
      REFERENCE/DOCKET NUMBER: 7MK-060548-00233
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 313-965-1976
      TELEFAX: 313-965-1951
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      TYPE: amino acid
      STRANDEDNESS: N/A
      TOPOLOGY: N/A
      MOLECULE TYPE: peptide
      ORIGINAL SOURCE:
      ORGANISM: N/A
      PUBLICATION INFORMATION:
      AUTHORS: N/A
      TITLE: N/A
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      US-08-436-703B-15

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RESULT 45
 US-08-436-703B-15
 Sequence 15, Application US/08436703B
 Patent No. 5919761
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR
 TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
 TITLE OF INVENTION: WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J, Rohm, Esq.
 STREET: 6601 Woodward Avenue
 STREET: Suite 1525
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America
 ZIP: 48226
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk 1.44mb, 3.5"
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 6/
 SOFTWARE: ASCII (DOS)Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436, 703B

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2005, 09:46:35 ; Search time 159 Seconds

(Without alignments)
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Perfect score: 105
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Gapop 10.0 , Gapext 0.5

Searched: 1726218 seqs, 38631768 residues
Total number of hits satisfying chosen parameters: 1726218

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	67	63.8	104	US-10-177-725-92	Sequence 92, Appl
3	67	63.8	104	US-10-393-449-42	Sequence 42, Appl
4	67	63.8	104	US-10-393-449-92	Sequence 92, Appl
5	66	62.9	827	US-10-437-963-152005	Sequence 152005, A
6	65.5	62.4	428	US-10-282-122A-5748	Sequence 5748, A
7	64	61.0	28	US-10-667-004-21	Sequence 21, Appl
8	64	61.0	28	US-10-667-004-24	Sequence 24, Appl
9	64	61.0	104	US-10-177-725-39	Sequence 39, Appl
10	64	61.0	104	US-10-177-725-40	Sequence 40, Appl
11	64	61.0	104	US-10-177-725-89	Sequence 89, Appl

12	64	61.0	104	14	US-10-177-725-90	Sequence 90, Appl
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15	64 <td>61.0<td>104</td><td>15<td>US-10-393-449-89<td>Sequence 89, Appl</td></td></td></td>	61.0 <td>104</td> <td>15<td>US-10-393-449-89<td>Sequence 89, Appl</td></td></td>	104	15 <td>US-10-393-449-89<td>Sequence 89, Appl</td></td>	US-10-393-449-89 <td>Sequence 89, Appl</td>	Sequence 89, Appl
16	64 <td>61.0<td>104</td><td>15<td>US-10-393-449-90<td>Sequence 90, Appl</td></td></td></td>	61.0 <td>104</td> <td>15<td>US-10-393-449-90<td>Sequence 90, Appl</td></td></td>	104	15 <td>US-10-393-449-90<td>Sequence 90, Appl</td></td>	US-10-393-449-90 <td>Sequence 90, Appl</td>	Sequence 90, Appl
17	63.5	60.5 <td>104</td> <td>14<td>US-10-177-725-41<td>Sequence 41, Appl</td></td></td>	104	14 <td>US-10-177-725-41<td>Sequence 41, Appl</td></td>	US-10-177-725-41 <td>Sequence 41, Appl</td>	Sequence 41, Appl
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23	63	60.0 <td>59</td> <td>15<td>US-10-393-449-55<td>Sequence 55, Appl</td></td></td>	59	15 <td>US-10-393-449-55<td>Sequence 55, Appl</td></td>	US-10-393-449-55 <td>Sequence 55, Appl</td>	Sequence 55, Appl
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31	63	60.0 <td>75</td> <td>15<td>US-10-393-449-53<td>Sequence 53, Appl</td></td></td>	75	15 <td>US-10-393-449-53<td>Sequence 53, Appl</td></td>	US-10-393-449-53 <td>Sequence 53, Appl</td>	Sequence 53, Appl
32	63	60.0 <td>75</td> <td>15<td>US-10-393-449-103<td>Sequence 103, Appl</td></td></td>	75	15 <td>US-10-393-449-103<td>Sequence 103, Appl</td></td>	US-10-393-449-103 <td>Sequence 103, Appl</td>	Sequence 103, Appl
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36	63	60.0 <td>83</td> <td>15<td>US-10-393-449-102<td>Sequence 102, Appl</td></td></td>	83	15 <td>US-10-393-449-102<td>Sequence 102, Appl</td></td>	US-10-393-449-102 <td>Sequence 102, Appl</td>	Sequence 102, Appl
37	63	60.0 <td>88</td> <td>14<td>US-10-177-725-99<td>Sequence 99, Appl</td></td></td>	88	14 <td>US-10-177-725-99<td>Sequence 99, Appl</td></td>	US-10-177-725-99 <td>Sequence 99, Appl</td>	Sequence 99, Appl
38	63	60.0 <td>88</td> <td>14<td>US-10-177-725-99<td>Sequence 99, Appl</td></td></td>	88	14 <td>US-10-177-725-99<td>Sequence 99, Appl</td></td>	US-10-177-725-99 <td>Sequence 99, Appl</td>	Sequence 99, Appl
39	63	60.0 <td>88</td> <td>15<td>US-10-393-449-49<td>Sequence 49, Appl</td></td></td>	88	15 <td>US-10-393-449-49<td>Sequence 49, Appl</td></td>	US-10-393-449-49 <td>Sequence 49, Appl</td>	Sequence 49, Appl
40	63	60.0 <td>88</td> <td>15<td>US-10-393-449-99<td>Sequence 99, Appl</td></td></td>	88	15 <td>US-10-393-449-99<td>Sequence 99, Appl</td></td>	US-10-393-449-99 <td>Sequence 99, Appl</td>	Sequence 99, Appl
41	63	60.0 <td>91</td> <td>14<td>US-10-177-725-51<td>Sequence 51, Appl</td></td></td>	91	14 <td>US-10-177-725-51<td>Sequence 51, Appl</td></td>	US-10-177-725-51 <td>Sequence 51, Appl</td>	Sequence 51, Appl
42	63	60.0 <td>91</td> <td>14<td>US-10-177-725-101<td>Sequence 101, Appl</td></td></td>	91	14 <td>US-10-177-725-101<td>Sequence 101, Appl</td></td>	US-10-177-725-101 <td>Sequence 101, Appl</td>	Sequence 101, Appl
43	63	60.0 <td>91</td> <td>15<td>US-10-393-449-51<td>Sequence 51, Appl</td></td></td>	91	15 <td>US-10-393-449-51<td>Sequence 51, Appl</td></td>	US-10-393-449-51 <td>Sequence 51, Appl</td>	Sequence 51, Appl
44	63	60.0 <td>91</td> <td>15<td>US-10-393-449-101<td>Sequence 101, Appl</td></td></td>	91	15 <td>US-10-393-449-101<td>Sequence 101, Appl</td></td>	US-10-393-449-101 <td>Sequence 101, Appl</td>	Sequence 101, Appl
45	63	60.0 <td>104</td> <td>14</td> <td>US-10-177-725-47<td>Sequence 47, Appl</td></td>	104	14	US-10-177-725-47 <td>Sequence 47, Appl</td>	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-177-725-42 Application US/10177725
Sequence 42, Appl
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177, 725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415, 765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169, 015
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: synthetic
US-10-177-725-42

Query Match 63.8%; Score 67; DB 14; Length 104;
Best Local Similarity 68.0%; Pred. No. 0.3;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AXAEAAKAAKAAKAAKAAKAAKAXA 25
Db 10 AAAAEEAAKAAKAAKAAKAAKAAEA 34

```
RESULT 2
US-10-177-725-92
; Sequence 92, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/RMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (37)..(68)
; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (37)..(68)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, 53-54, 56-58, 60-6
; OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (37)..(68)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, 53-54, 56-58, 60-6
; OTHER INFORMATION: 2, 64-65, and 67-69 can be any amino acid
US-10-177-725-92

Query Match          63.8%; Score 67; DB 14; Length 104;
Best Local Similarity 68.0%; Pred. No. 0.3;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY      1 AXAAAEKAKYAAAEAKAKAXA 25
Db      10 AAAAAEAAKAAAEAAKAAAEAA 34

RESULT 3
US-10-393-449-42
; Sequence 42, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-393-449-42
```

```
Query Match          63.8%; Score 67; DB 15; Length 104;
Best Local Similarity 68.0%; Pred. No. 0.3;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY      1 AXAAAEKAKYAAAEAKAKAXA 25
Db      10 AAAAAEAAKAAAEAAKAAAEAA 34

RESULT 4
US-10-393-449-92
; Sequence 92, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (37)..(68)
; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
; OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (37)..(68)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, 53-54, 56-58, 60-6
; OTHER INFORMATION: 2, 64-65, and 67-69 can be any amino acid
US-10-393-449-92

Query Match          63.8%; Score 67; DB 15; Length 104;
Best Local Similarity 68.0%; Pred. No. 0.3;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY      1 AXAAAEKAKYAAAEAKAKAXA 25
Db      10 AAAAAEAAKAAAEAAKAAAEAA 34

RESULT 5
US-10-437-963-152005
; Sequence 152005, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: Ia Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
```

```

; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152005
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52099C.1.pep
US-10-437-963-152005

Query Match          62.9%; Score 66; DB 16; Length 827;
Best Local Similarity 54.5%; Pred. No. 4;
Matches 18; Conservative 4; Mismatches 3; Indels 8; Gaps 1;

Oy      1 AXAAAEKAAKAA-----EAAEKAAKAXA 25
Db      398 AAARERRAAKAAAEAKERVAAERARRAKAA 430

RESULT 6
US-10-282-122A-55748
; Sequence 55748, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Hsiangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/251,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55748
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-55748

Query Match          62.4%; Score 65.5; DB 15; Length 428;
Best Local Similarity 62.1%; Pred. No. 2.2;
Matches 18; Conservative 4; Mismatches 2; Indels 5; Gaps 1;
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Oy      1 AXAAAEKAA-----KYAAAEKAAKAX 24
Db      210 AAEAAKKAQAQAEKKAABAAKAAABAE 238

RESULT 7
US-10-667-004-21
; Sequence 21, Application US/10667004
; Publication No. US20040126820A1
; GENERAL INFORMATION:
; APPLICANT: INTEL CORPORATION
; APPLICANT: CHAN, Selena
; APPLICANT: SU, Xing
; APPLICANT: YAMAKAWA, Mineo
; TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
; FILE REFERENCE: INTEL1310-1(P14240X)
; CURRENT APPLICATION NUMBER: US/10/667,004
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 10/251,152
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-667-004-21

Query Match          61.0%; Score 64; DB 16; Length 28;
Best Local Similarity 65.2%; Pred. No. 0.17;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy      2 XAAAEKAAKAAAEAKAAKAX 24
Db      1 AAARAAARAAARAAARAAARAA 23

RESULT 8
US-10-667-004-24
; Sequence 24, Application US/10667004
; Publication No. US20040126820A1
; GENERAL INFORMATION:
; APPLICANT: INTEL CORPORATION
; APPLICANT: CHAN, Selena
; APPLICANT: SU, Xing
; APPLICANT: YAMAKAWA, Mineo
; TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
; FILE REFERENCE: INTEL1310-1(P14240X)
; CURRENT APPLICATION NUMBER: US/10/667,004
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 10/251,152
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-667-004-24

Query Match          61.0%; Score 64; DB 16; Length 28;
Best Local Similarity 65.2%; Pred. No. 0.17;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

Db 1 AAATAAATAAATAAATAAATAA 23

RESULT 9

US-10-177-725-39
; Sequence 39, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-177-725-39

Query Match 61.0%; Score 64; DB 14; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.73;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 AXAAEAERAKYAAEAERAKAXA 25
Db 9 AAATAAATAA--AAATAAATAA 31

RESULT 10

US-10-177-725-40
; Sequence 40, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-177-725-40

Query Match 61.0%; Score 64; DB 14; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.73;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 AXAAEAERAKYAAEAERAKAXA 25
Db 9 AAATAAATAA--AAATAAATAA 31

RESULT 11

US-10-177-725-89
; Sequence 89, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (37)-(68)
; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
; OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
US-10-177-725-89

Query Match 61.0%; Score 64; DB 14; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.73;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 AXAAEAERAKYAAEAERAKAXA 25
Db 9 AAATAAATAA--AAATAAATAA 31

RESULT 12

US-10-177-725-90
; Sequence 90, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (37)-(68)
; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
; OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
US-10-177-725-90

Query Match 61.0%; Score 64; DB 14; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.73;

Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
Qy 1 AXAEAAEKAAKYAAAEAAEKAAKAXA 25
|:||||| ||| ||||| |
Db 9 AAEEAAAKAA--AAAAEAAAKAA 31

RESULT 13
US-10-393-449-39

; Sequence 39, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-393-449-39

Query Match 61.0%; Score 64; DB 15; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.73;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 AXAEAAEKAAKYAAAEAAEKAAKAXA 25
|:||||| ||| ||||| |
Db 9 AAEEAAAKAA--AAAAEAAAKAA 31

RESULT 14
US-10-393-449-40

; Sequence 40, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-393-449-40

Query Match 61.0%; Score 64; DB 15; Length 104;

Best Local Similarity 72.0%; Pred. No. 0.73;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 AXAEAAEKAAKYAAAEAAEKAAKAXA 25
|:||||| ||| ||||| |
Db 9 AAEEAAAKAA--AAAAEAAAKAA 31

RESULT 15
US-10-393-449-89

; Sequence 89, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (337)-(68)
; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
; OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
US-10-393-449-89

Query Match 61.0%; Score 64; DB 15; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.73;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 AXAEAAEKAAKYAAAEAAEKAAKAXA 25
|:||||| ||| ||||| |
Db 9 AAEEAAAKAA--AAAAEAAAKAA 31

RESULT 16
US-10-393-449-90

; Sequence 90, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 104
; TYPE: PRT

ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (37)..(68)
OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
US-10-393-449-90

Query Match 61.0%; Score 64; DB 15; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.73;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 AXAAEAERKAKYAAEAERKAKAXA 25
Db 9 AAAAEEAAKAA--AAAAEAERKAKAA 31

RESULT 17
US-10-177-725-41
Sequence 41, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-177-725-41

Query Match 60.5%; Score 63.5; DB 14; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.85;
Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 AXAAEAERKAKYAAEAERKAKAXA 25
Db 6 AAAAEEAAKAA--AAAAEAERKAKAA 29

RESULT 18
US-10-177-725-91
Sequence 91, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 91

LENGTH: 104
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (37)..(68)
OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
US-10-177-725-91

Query Match 60.5%; Score 63.5; DB 14; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.85;
Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 AXAAEAERKAKYAAEAERKAKAXA 25
Db 6 AAAAEEAAKAA--AAAAEAERKAKAA 29

RESULT 19
US-10-393-449-41
Sequence 41, Application US/10393449
Publication No. US20030224412A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-393-449-41

Query Match 60.5%; Score 63.5; DB 15; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.85;
Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 AXAAEAERKAKYAAEAERKAKAXA 25
Db 6 AAAAEEAAKAA--AAAAEAERKAKAA 29

RESULT 20
US-10-393-449-91
Sequence 91, Application US/10393449
Publication No. US20030224412A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765

```

Query Match Similarity      60.0%; Score 63; DB 14; Length 59;
Best Local Similarity      66.7%; Pred. No. 0.53;
Matches      16; Conservative      2; Mismatches      6; Indels      0; Gaps      0;

OY      2 XAEAAEKAKYTAEEAEKAKAXA 25
      : ||| ||| ||| ||| ||| :
      4 DAAAAEAAAKAAEAEMAAAEAA 27

RESULT 22
US-10-177-725-105
; Sequence 105, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Bear R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177.725

```

```

Query Match      60.0%; Score 63; DB 15; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.53;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0

OY      2 XAEAAEKAKYAAEAEEKATAXA 25
      : ||| ||| ||| ||| : |
Db      4 DAAAEAAAKAAAEAAKAAAEAA 27

RESULT 24
US-10-393-449-105
; Sequence 105, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenderger, Jakob M.

```

```
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 105
LENGTH: 59
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
NAME/KEY: MISC FEATURE
LOCATION: (30)-(46)
OTHER INFORMATION: "Xaa" at positions 30-32, 34-36, 38-39, 41-43, and 45-46 can be a
OTHER INFORMATION: ny amino acid
US-10-393-449-105
```

```
Query Match          60.0%; Score 63; DB 15; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.53;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      2 XAEAEKAKYAAAEAKAKAXA 25
       :| ||| ||| ||| ||| ||| :|
Db      4 DAAAEAAAKAAAEAAKAAAEAA 27
```

```
RESULT 25
US-10-177-725-54
Sequence 54, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-177-725-54
```

```
Query Match          60.0%; Score 63; DB 14; Length 67;
Best Local Similarity 66.7%; Pred. No. 0.61;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      2 XAEAEKAKYAAAEAKAKAXA 25
       :| ||| ||| ||| ||| ||| :|
Db      4 DAAAEAAAKAAAEAAKAAAEAA 27
```

```
RESULT 26
US-10-177-725-104
Sequence 104, Application US/10177725
```

```
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
NAME/KEY: MISC FEATURE
LOCATION: (38)-(54)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
OTHER INFORMATION: ny amino acid
US-10-177-725-104
```

```
Query Match          60.0%; Score 63; DB 14; Length 67;
Best Local Similarity 66.7%; Pred. No. 0.61;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      2 XAEAEKAKYAAAEAKAKAXA 25
       :| ||| ||| ||| ||| ||| :|
Db      4 DAAAEAAAKAAAEAAKAAAEAA 27
```

```
RESULT 27
US-10-393-449-54
Sequence 54, Application US/10393449
Publication No. US20030224412A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-393-449-54
```

```
Query Match          60.0%; Score 63; DB 15; Length 67;
Best Local Similarity 66.7%; Pred. No. 0.61;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      2 XAEAEKAKYAAAEAKAKAXA 25
       :| ||| ||| ||| ||| ||| :|
Db      4 DAAAEAAAKAAAEAAKAAAEAA 27
```

```
RESULT 28
US-10-393-449-104
; Sequence 104, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (38)..(54)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
; OTHER INFORMATION: ny amino acid
US-10-393-449-104

Query Match      60.0%; Score 63; DB 15; Length 67;
Best Local Similarity 66.7%; Pred. No. 0.61;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      2 XAEEAKAKYAAEAEAKAKAXA 25
      : ||| ||| ||| ||| ||| :
      4 DAAAAEAAKAAAEAAKAAAEAA 27

Db
US-10-177-725-53
; Sequence 53, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-177-725-53

Query Match      60.0%; Score 63; DB 14; Length 75;
Best Local Similarity 66.7%; Pred. No. 0.69;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      2 XAEEAKAKYAAEAEAKAKAXA 25
      : ||| ||| ||| ||| ||| :
      4 DAAAAEAAKAAAEAAKAAAEAA 27

Db
US-10-393-449-103
; Sequence 103, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (38)..(54)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
; OTHER INFORMATION: ny amino acid
US-10-177-725-103

Query Match      60.0%; Score 63; DB 14; Length 75;
Best Local Similarity 66.7%; Pred. No. 0.69;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      2 XAEEAKAKYAAEAEAKAKAXA 25
      : ||| ||| ||| ||| ||| :
      4 DAAAAEAAKAAAEAAKAAAEAA 27

Db
US-10-393-449-53
; Sequence 53, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-393-449-53
```

Query Match 60.0%; Score 63; DB 15; Length 75;
Best Local Similarity 66.7%; Pred. No. 0.69;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAAAEKAKYAAEAERAKAKAXA 25
DB 4 DAAAEAAAKAAEAERAKAAEA 27

RESULT 32
US-10-393-449-103
Sequence 103, Application US/10393449
Publication No. US20030224412A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenderger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 103
LENGTH: 75
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
NAME/KEY: MISC_FEATURE
LOCATION: (38)-(54)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
US-10-393-449-103

Query Match 60.0%; Score 63; DB 15; Length 75;
Best Local Similarity 66.7%; Pred. No. 0.69;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAAAEKAKYAAEAERAKAKAXA 25
DB 4 DAAAEAAAKAAEAERAKAAEA 27

RESULT 33
US-10-177-725-52
Sequence 52, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenderger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: A-66900-4/RMS/AWS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52
LENGTH: 83
TYPE: PRT
ORGANISM: Artificial sequence

FEATURE:
OTHER INFORMATION: synthetic
US-10-177-725-52

Query Match 60.0%; Score 63; DB 14; Length 83;
Best Local Similarity 66.7%; Pred. No. 0.77;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAEEAEKAKYAAEAERAKAKAX 24
DB 57 AAKAAEAERAKAAEAERAKAAK 80

RESULT 34
US-10-177-725-102
Sequence 102, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenderger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: A-66900-4/RMS/AWS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 102
LENGTH: 83
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
NAME/KEY: MISC_FEATURE
LOCATION: (38)-(54)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
US-10-177-725-102

Query Match 60.0%; Score 63; DB 14; Length 83;
Best Local Similarity 66.7%; Pred. No. 0.77;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAEEAEKAKYAAEAERAKAKAX 24
DB 57 AAKAAEAERAKAAEAERAKAAK 80

RESULT 35
US-10-393-449-52
Sequence 52, Application US/10393449
Publication No. US20030224412A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenderger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1

SEQ ID NO 52
LENGTH: 83
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-393-449-52

Query Match 60.0%; Score 63; DB 15; Length 83;
Best Local Similarity 66.7%; Pred. No. 0.77;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAEAEKAKYAAAEAKAKAX 24
Db 57 AAKAAAEAAKAAAEAAKAAK 80

RESULT 36
US-10-393-449-102
Sequence 102, Application US/10393449
Publication No. US20030224412A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.

TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: RIGL-007CIP3
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 102
LENGTH: 83
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (38)-(54)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
OTHER INFORMATION: my amino acid
US-10-393-449-102

Query Match 60.0%; Score 63; DB 15; Length 83;
Best Local Similarity 66.7%; Pred. No. 0.77;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAEAEKAKYAAAEAKAKAX 24
Db 57 AAKAAAEAAKAAAEAAKAAK 80

RESULT 37
US-10-177-725-49
Sequence 49, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.

TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT FILING DATE: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08

PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
LENGTH: 88
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-177-725-49

Query Match 60.0%; Score 63; DB 14; Length 88;
Best Local Similarity 66.7%; Pred. No. 0.82;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAEAEKAKYAAAEAKAKAX 24
Db 63 AAKAAAEAAKAAAEAAKAAK 86

RESULT 38
US-10-177-725-99
Sequence 99, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.

TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US/10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
LENGTH: 88
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (29)-(60)
OTHER INFORMATION: "Xaa" at positions 29-31, 33-35, 37-38, 40-42, 44-45, 47-49, 51-5
OTHER INFORMATION: 3, 55-56, and 58-60 can be any amino acid
US-10-177-725-99

Query Match 60.0%; Score 63; DB 14; Length 88;
Best Local Similarity 66.7%; Pred. No. 0.82;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAEAEKAKYAAAEAKAKAX 24
Db 63 AAKAAAEAAKAAAEAAKAAK 86

RESULT 39
US-10-393-449-49
Sequence 49, Application US/10393449
Publication No. US20030224412A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.

TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: RIGL-007CIP3
CURRENT FILING DATE: US/10/393,449
CURRENT FILING DATE: 2003-03-18

```

1 PRIOR APPLICATION NUMBER: US 10/177,725
2 PRIOR FILING DATE: 2002-06-20
3 PRIOR APPLICATION NUMBER: US 09/415,765
4 PRIOR FILING DATE: 1999-10-08
5 PRIOR APPLICATION NUMBER: US 09/169,015
6 PRIOR FILING DATE: 1998-10-08
7 NUMBER OF SEQ ID NOS: 173
8 SOFTWARE: PatentIn version 3.1
9 SEQ ID NO 49
10 LENGTH: 88
11 TYPE: DRT
12 ORGANISM: Artificial sequence
13 FEATURE:
14 OTHER INFORMATION: synthetic
15 US-10-393-449-49

```

Query Match	60.0%;	Score 63;	DB 15;	Length 88;
Best Local Similarity	66.7%;	Pred. No. 0.82;		
Matches	16;	Conservative	2;	Mismatches 6;
				Indels 0;
				Gaps 0;

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QY      1 AAAGAAEKAAKYAAEAEEKAAX 24
          | : | | | | | | | | :
Db      63 AAKAAAEAAAKAAAEAAAKAAAK 86

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RESULT 40
US-10-393-449-99
Sequence 99, Application US/10393449
Publication NO. US20030224412M1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenderger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIORITY APPLICATION NUMBER: US 10/177,725
PRIORITY FILING DATE: 2002-06-20
PRIORITY APPLICATION NUMBER: US 09/415,765
PRIORITY FILING DATE: 1999-10-08
PRIORITY APPLICATION NUMBER: US 09/169,015
PRIORITY FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
LENGTH: 88
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (29)..(60)
OTHER INFORMATION: "xaa" at positions 29-31, 33-35, 37-38, 40-42, 44-45, 47-49, 51-5
US-10-393-449-99

```

Query Match	60.0%;	Score 63;	DB 15;	Length 88;
Best Local Similarity	66.7%;	Pred. No. 0.82;		
Matches 16;	Conservative 2;	Mismatches 6;	Indels 0;	Gaps 0;

QY 1 AAAGAAEKAAYAAEAAEKAAX 24
| : | | | | | | | | :
Db 63 AAAGAAEAAAKAAEAAAKAAAK 86

```

RESULT 41
US-10-177-725-51
; Sequence 51, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David

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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peelle, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SEQUENCES
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51
LENGTH: 91
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-177-725-51

```

Query Match	60.0%	Score 63;	DB 14;	Length 91;
Best Local Similarity	66.7%	Pred. No. 0.85;		
Matches 16;	Conservative 2;	Mismatches 6;	Indels 0;	Gaps 0

QY 1 AXAEAEKAAKYAAEEAEKAAKAX 24
| : ||| ||| ||| ||| :
Db 65 AAATAAEAAAKAAAEAAAKAAAK 88

```

RESULT 42
US-10-177-725-101
; Sequence 101, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (38) -(54)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
; OTHER INFORMATION: my amino acid
US-10-177-725-101

```

Query Match 60.0%; Score 63; DB 14; Length 91;
 Best Local Similarity 66.7%; Pred. No. 0.85;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AXAEAEKAAKYAAEAAEKAKAX 24
| : ||| ||| ||| ||| :
Db 65 AAKAAAEAAAKAAAEAAAKAAAK 88

RESULT 43
US-10-393-449-51
; Sequence 51, Application US/10393445
; Publication No. US20030224412A1

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-393-449-51

Query Match          60.0%; Score 63; DB 15; Length 91;
Best Local Similarity 66.7%; Pred. No. 0.85;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAAEAERKAKYAAEAERKAKAX 24
   |:|||||:|||||:|||||:
Db 65 AAKAAAEAAKAAAEAAKAAKAAK 88

RESULT 44
US-10-393-449-101
; Sequence 101, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
NAME/KEY: MISC_FEATURE
LOCATION: (38)..(54)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
; OTHER INFORMATION: my amino acid
US-10-393-449-101

Query Match          60.0%; Score 63; DB 15; Length 91;
Best Local Similarity 66.7%; Pred. No. 0.85;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAAEAERKAKYAAEAERKAKAX 24
   |:|||||:|||||:|||||:
Db 65 AAKAAAEAAKAAAEAAKAAKAAK 88
```

```
RESULT 45
US-10-177-725-47
; Sequence 47, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
; FILE REFERENCE: A-66900-4/RMS/RMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-177-725-47

Query Match          60.0%; Score 63; DB 14; Length 104;
Best Local Similarity 66.7%; Pred. No. 0.98;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 AXAAEAERKAKYAAEAERKAKAX 24
   |:|||||:|||||:|||||:
Db 79 AAKAAAEAAKAAAEAAKAAKAAK 102

Search completed: July 11, 2005, 10:00:02
Job time : 160 secs
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